

[illegible]

1

[REDACTED]

[illegible]

FIGURE 1C

1000000	TCCAGCCCCACATCGAXGACCTGAXCCGTCTCCTGGGAGCCTXTCGCCAGGTGCCGACCGGACCTGCCCCCTGGCA	
1000000	T.....C..T...A.....C..CC..A.....	764
1000000	GGG.....C..C...GGC..T...C..A...T...A...T...	761
1000000C.....A.....C..G.....T.....C.....C.....	770
1000000	GCCTGCACCTCCGCCAAGXGCCCGGAGCGCCGACCGCGGCTTACGGCCCTTCTCGAGAGCGCTGGACCTT	
1000000AA.....A.....A.....T.....T.....T.....T.....T.....	834
1000000GG..C..C..C..GACA...A...T.....T...GG...T...C...T.....	831
1000000C.....C..G.....C.....C.....C.....C.....C.....C.....	840
1000000	CGCAGCGTCTCTCCACCGAGTTCCGGCTCTGAGAGCGCCGCAAGGCCCTCGAGCGGCGCCCTCGCCCGCGCGC	
1000000T.....AA.....T.....T.....T.....T.....T.....	904
1000000C.....C.....C.....C.....C.....C.....C.....C.....	901
1000000C.....C.....C.....C.....C.....C.....C.....C.....	910
1000000	CGCAGCGCGCGCTTCGTGGGCTTGTCTTTCGGCGCCGCGGCACTGCGCGCGGCTTCGCGCGCTGGC	
1000000G.....AAG.....T.....T.....T.....T.....T.....	974
1000000T...TT.....TC..T.....T.....T.....T.....T.....T.....	971
1000000C.....C.....C.....C.....C.....C.....C.....C.....	980
1000000	CGCCCGCGAGCGCGCGCTCCACCGCGGACCGAGACCGCTTAXGGCGCTXAGCGGAGCTXAACCGAGCTG	
1000000C.....C.....C.....C.....C.....C.....C.....C.....	1044
1000000G...GT.....G..CC...T.....A.....C.....C.....T.....C.....	1041
1000000TC.....C.....C.....C.....C.....C.....C.....C.....	1050

FIGURE 1E

5'...	GGAGATCCCGCCCGCTCCAGGAGCAGCGTCTCCGGCTGCGCGGCGCAGCCCTCAACCTCAAGTCCCGGGAG	1464
3'...	CC...	1461
5'...	GCG...ACGCG...T...G...	1470
3'...	...	
5'...	CAGCTCGAAGCGTGGTCTTTCAGCAAGCTXGCGGCTTCCCGCCATCCGGCAAGACGGAGACXGGCAAGC	1534
3'...	A...A...C...	1531
5'...	GC...GCG...T...T...G...CA...A...	1540
3'...	TA...T...G...A...	
5'...	CCTCAGCAGCGCGCGCTGCTCGAGCGCGCTXGCGAGCGCGCCACCCCATCGTGGAGAAAGATCGTCGAGTA	1604
3'...	C...C...G...C...C...C...	1601
5'...	T...T...A...G...G...G...G...G...G...	1610
3'...	G...G...A...G...G...G...G...G...G...	
5'...	CCCGGACCTCAGCAAGCTCAGCAACACCTAGATXGACCGCGCTCCCGXGCGTGGTCCACCCGACGACGGGG	1674
3'...	G...G...T...T...G...A...A...A...A...A...	1671
5'...	...	1680
3'...	...	
5'...	CGCCTCGACACCGGCTTCAACCAAGACGGCGACGGCGGCGGCGCTTACCTCCGACCGCAACCTCC	1744
3'...	A...T...T...T...T...T...T...T...T...	1741
5'...	...	1750
3'...	...	

FIGURE 1F

SEQUENCE	AGAACATCGCCGTCGCCACCCXCTCGCCACAGAGCATCCGCGCGGCCCTTCGTCGCCGACGACGCGXTCGGC	
SEQUENCEG..T..G.....A..C.....C...C..	1914
SEQUENCEG.....T.....C..C.....A.....C.....	1911
SEQUENCEC.....C.....C.....C.....C.....T.....C.....	1920
SEQUENCE	GTTCGTCGCCGCTCGACCTATACCCAGATAGAGCTCGCGGTCCTCGCCGACGCTCGCGCGGACGACGACCTG	
SEQUENCEA.....G.....A.....G.....C.....	1984
SEQUENCEC.....T.....T.....T.....C.....	1981
SEQUENCEC.....C.....C.....C.....A.....	1990
SEQUENCE	ATCCCGGCTCTCCAGGCGGCGGACATCCAGACCCAGACCCGCGAGCTCGCATCTTCGCGGCTCGCCCGCGG	
SEQUENCEC.....G.....GG.....G.....G.....	1954
SEQUENCET.....T.....T.....T.....T.....	1951
SEQUENCEA.....A.....A.....A.....A.....	1960
SEQUENCE	ACCGCGCTCGACCGCGCTGATCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	
SEQUENCEA.....A.....A.....A.....A.....	2024
SEQUENCEG.....G.....G.....G.....G.....	2021
SEQUENCEG.....G.....G.....G.....G.....	2030
SEQUENCE	CCACCGCGCTCTCCAGGCGGCTTCGATCGCGGCTACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	
SEQUENCEA.....A.....T.....CCA.....T.....	2094
SEQUENCEGG.....T.....T.....T.....T.....	2091
SEQUENCETA..G.....T.....T.....T.....A.....	2100

[REDACTED]

SEQUENCE	POSITION	BASE
ACCTTCCCCAAAGCTGCGCGCGCTGGATTGACAAAGACCGCTGCAGGAGCGCCAGCGCGCGCGGTACCTGGAGAG	2164	
.....	2165	
.....	2166	
.....	2167	
.....	2168	
.....	2169	
.....	2170	
.....	2171	
.....	2172	
.....	2173	
.....	2174	
.....	2175	
.....	2176	
.....	2177	
.....	2178	
.....	2179	
.....	2180	
.....	2181	
.....	2182	
.....	2183	
.....	2184	
.....	2185	
.....	2186	
.....	2187	
.....	2188	
.....	2189	
.....	2190	
.....	2191	
.....	2192	
.....	2193	
.....	2194	
.....	2195	
.....	2196	
.....	2197	
.....	2198	
.....	2199	
.....	2200	
.....	2201	
.....	2202	
.....	2203	
.....	2204	
.....	2205	
.....	2206	
.....	2207	
.....	2208	
.....	2209	
.....	2210	
.....	2211	
.....	2212	
.....	2213	
.....	2214	
.....	2215	
.....	2216	
.....	2217	
.....	2218	
.....	2219	
.....	2220	
.....	2221	
.....	2222	
.....	2223	
.....	2224	
.....	2225	
.....	2226	
.....	2227	
.....	2228	
.....	2229	
.....	2230	
.....	2231	
.....	2232	
.....	2233	
.....	2234	
.....	2235	
.....	2236	
.....	2237	
.....	2238	
.....	2239	
.....	2240	
.....	2241	
.....	2242	
.....	2243	
.....	2244	
.....	2245	
.....	2246	
.....	2247	
.....	2248	
.....	2249	
.....	2250	
.....	2251	
.....	2252	
.....	2253	
.....	2254	
.....	2255	
.....	2256	
.....	2257	
.....	2258	
.....	2259	
.....	2260	
.....	2261	
.....	2262	
.....	2263	
.....	2264	
.....	2265	
.....	2266	
.....	2267	
.....	2268	
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.....	2270	
.....	2271	
.....	2272	
.....	2273	
.....	2274	
.....	2275	
.....	2276	
.....	2277	
.....	2278	
.....	2279	
.....	2280	
.....	2281	
.....	2282	
.....	2283	
.....	2284	
.....	2285	
.....	2286	
.....	2287	
.....	2288	
.....	2289	
.....	2290	
.....	2291	
.....	2292	
.....	2293	
.....	2294	
.....	2295	
.....	2296	
.....	2297	
.....	2298	
.....	2299	
.....	2300	
.....	2301	
.....		

[REDACTED]

FIGURE 1H

5' GCGGCTGGAGGCTGGAGGCTGGGCAAGCGGAGGAGCTGGCTGTCGGGCAAGGAGCTAG	2499
3'	2496
..... GA	2505
..... CC.....	
..... T..... GT...	
.....	

3' GCGGCTGGAGGCTGGAGGCTGGGCAAGCGGAGGAGCTGGCTGTCGGGCAAGGAGCTAG

FIGURE 2A

1000000	MSAHLPLFEPKQAVLLVDGHHLAYRIFFAIKOLITSRCEPVQAVYGFASKLLKALKEDG·QAVXVVFDAK	
1001000H.....	69
1002000V.....	88
1003000YK..F.....	70
1004000	APSFRHEAYEAYKAGRPTPEOFPROLALIKELVOLLCXRLEVPGYEADDVLATLAKKAEEKGYEVRI L	
1005000A.....S.....	139
1006000V.....F.....R.....	138
1007000F.....	140
1008000	IA DRDLYOLLSORI AVLHPEGYLI TPWLWEKYGLRPEQWVDYRALXGDPSPDHLPQVKGIGEXIAXKLLX	
1009000H.....D.....T.....E.....R.....E	209
1010000Y.....A.....I.....	208
1011000H.....E.....F.....V.....L.....X	210
1012000	EVGSLLENLLKHLDRVKP·XXREKI XAHNEOLXLSXXLSXVRIOPLPLEVOFAXAREPDREGRAFLERLEF	
1013000L.....A.....D.....K.....WD.AK.....K.....R.....	278
1014000SL...LO.C...A.A...AK...O.H.....CR..T..IL.....	277
1015000EHV...K..L...R..LE..R.....L..OC.....	280
1016000	GSLLHEFGLLXPKALEEAPWPPPECAFVGFVLSRPEPMVAELLALAAARXGRVHRAXDPLXGLROLKEV	
1017000S.....K.....D.....G.....PE.YKA.....A	348
1018000G...A.....L..SF.....O.WE..L...Q...R.....G.	347
1019000A.AP.....X.....C.D.....A...A..K.....	350

FIGURE 2B

400	AGLLAKOLAVLALREGLQLXPGDDPMLLAYLLDPSNITPEGVARAYGGEWTEOACERALLSERLFXHLXX	
405S.....G.P.....E.....A.....A.....WC	418
410I.....F.E.....A.....A.....QT.KE	417
415S.....V.....AH.....HA.....LX	420
420R.....E.....A.....A.....A.....A.....	
425K.....K.....K.....K.....K.....K.....	
430K.....K.....K.....K.....K.....K.....	
435K.....K.....K.....K.....K.....K.....	
440K.....K.....K.....K.....K.....K.....	
445K.....K.....K.....K.....K.....K.....	
450K.....K.....K.....K.....K.....K.....	
455K.....K.....K.....K.....K.....K.....	
460K.....K.....K.....K.....K.....K.....	
465K.....K.....K.....K.....K.....K.....	
470K.....K.....K.....K.....K.....K.....	
475K.....K.....K.....K.....K.....K.....	
480K.....K.....K.....K.....K.....K.....	
485K.....K.....K.....K.....K.....K.....	
490K.....K.....K.....K.....K.....K.....	
495K.....K.....K.....K.....K.....K.....	
500K.....K.....K.....K.....K.....K.....	
505K.....K.....K.....K.....K.....K.....	
510K.....K.....K.....K.....K.....K.....	
515K.....K.....K.....K.....K.....K.....	
520K.....K.....K.....K.....K.....K.....	
525K.....K.....K.....K.....K.....K.....	
530K.....K.....K.....K.....K.....K.....	
535K.....K.....K.....K.....K.....K.....	
540K.....K.....K.....K.....K.....K.....	
545K.....K.....K.....K.....K.....K.....	
550K.....K.....K.....K.....K.....K.....	
555K.....K.....K.....K.....K.....K.....	
560K.....K.....K.....K.....K.....K.....	
565K.....K.....K.....K.....K.....K.....	
570K.....K.....K.....K.....K.....K.....	
575K.....K.....K.....K.....K.....K.....	
580K.....K.....K.....K.....K.....K.....	
585K.....K.....K.....K.....K.....K.....	
590K.....K.....K.....K.....K.....K.....	
595K.....K.....K.....K.....K.....K.....	
600K.....K.....K.....K.....K.....K.....	
605K.....K.....K.....K.....K.....K.....	
610K.....K.....K.....K.....K.....K.....	
615K.....K.....K.....K.....K.....K.....	
620K.....K.....K.....K.....K.....K.....	
625K.....K.....K.....K.....K.....K.....	
630K.....K.....K.....K.....K.....K.....	
635K.....K.....K.....K.....K.....K.....	
640K.....K.....K.....K.....K.....K.....	
645K.....K.....K.....K.....K.....K.....	
650K.....K.....K.....K.....K.....K.....	
655K.....K.....K.....K.....K.....K.....	
660K.....K.....K.....K.....K.....K.....	
665K.....K.....K.....K.....K.....K.....	
670K.....K.....K.....K.....K.....K.....	
675K.....K.....K.....K.....K.....K.....	
680K.....K.....K.....K.....K.....K.....	
685K.....K.....K.....K.....K.....K.....	
690K.....K.....K.....K.....K.....K.....	
695K.....K.....K.....K.....K.....K.....	
700K.....K.....K.....K.....K.....K.....	

FIGURE 2C

SEQUENCE	SFPKVRRAWIEXTLSEGRARROYVETLFGARRYPOLNARUKSVREAAERNAFHHPVOGIAADLHKLAHVXL	768
769E.....	767
770	Y.....G.....R.....	770
771K.....	
SEQUENCE	FPRLXEWGARNLLOVHDELVLAPKXRAEXVAALAKENVMEGVYPLAVPLEVEVQXGEDWLSAKEX	
830E.....A.....R.....	833
831D.....R.....W.....Q.....L.....	831
832L.....OA.....E.....A.....KA.....H.....G.....	835
833R.....L.....	

FIGURE 3

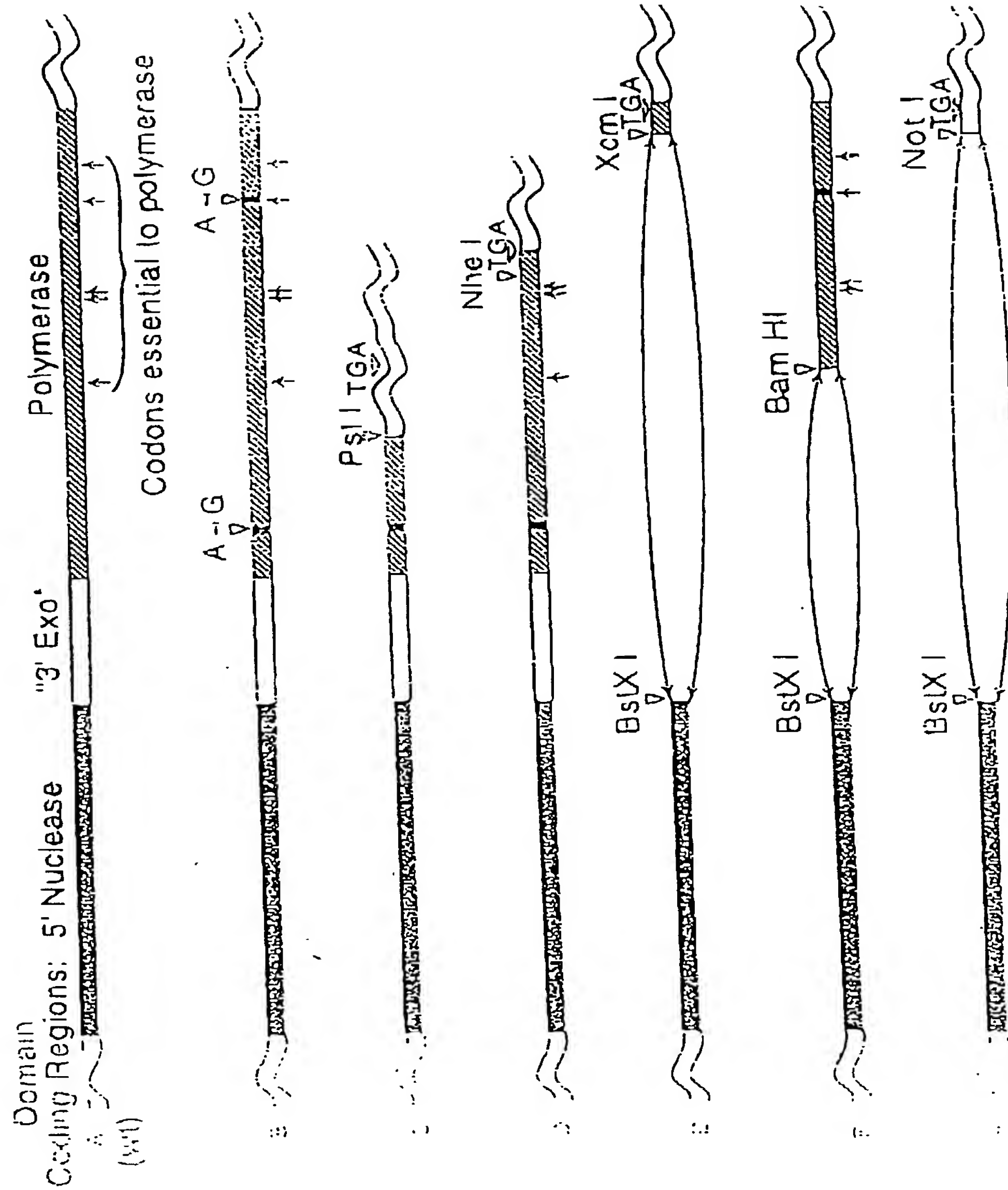


FIGURE 4

Genes for Wild-Type and Pol(-) DNAPTH

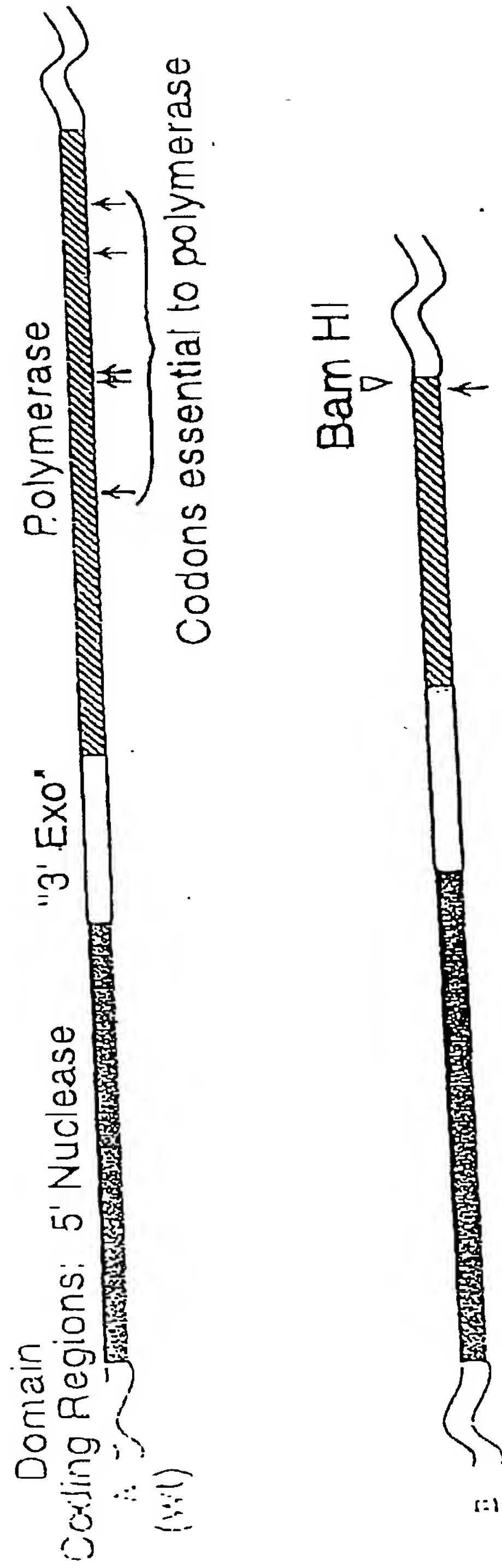
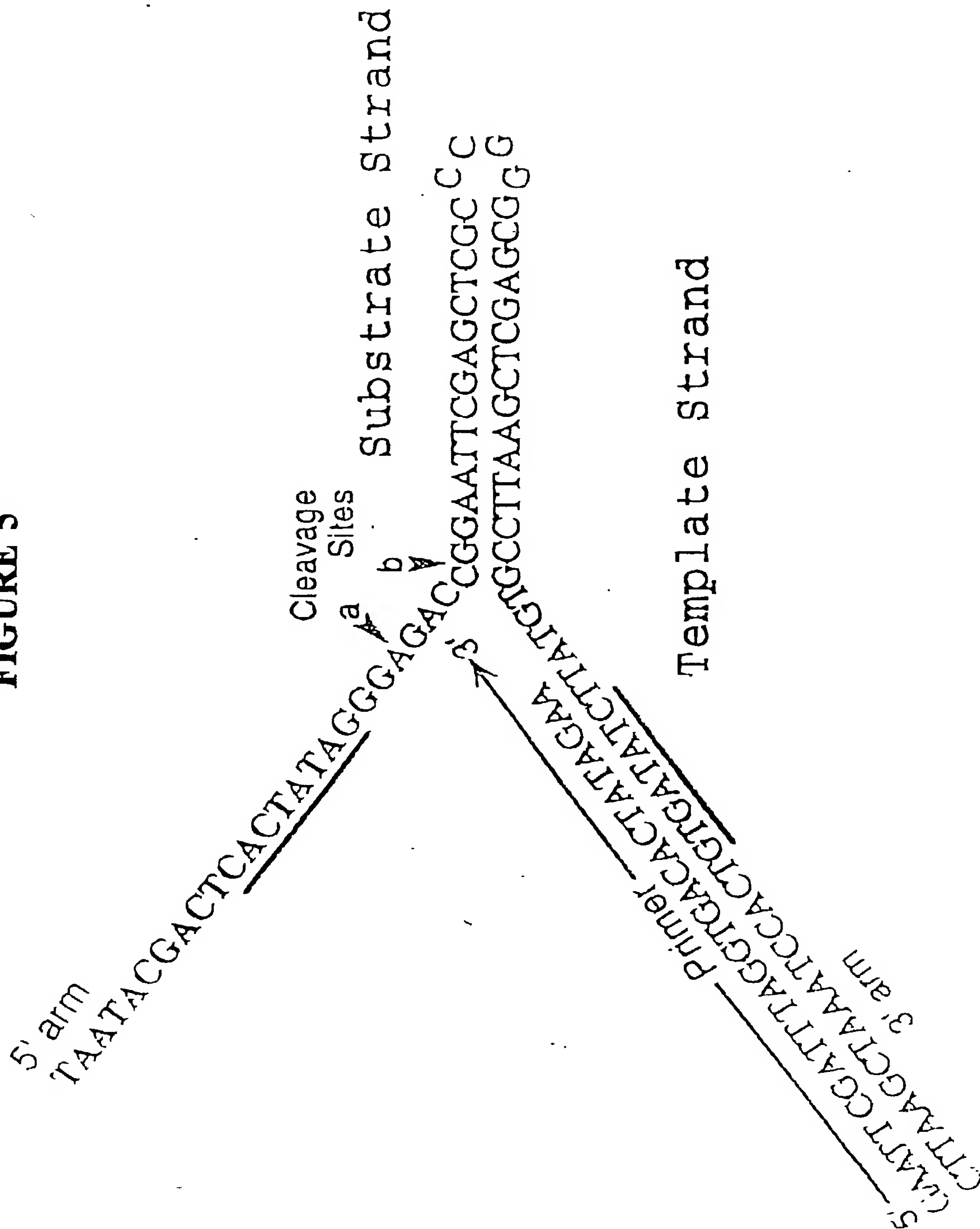


FIGURE 5



DNAP
TARGET
DNA

M T S M

 — + — +

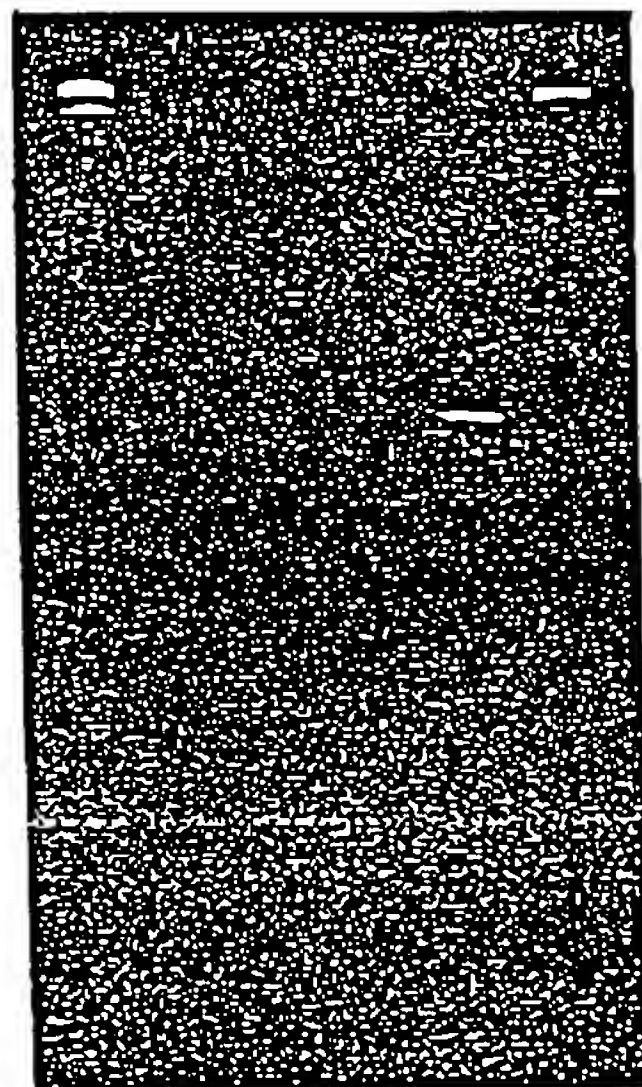


FIGURE 6

15.

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

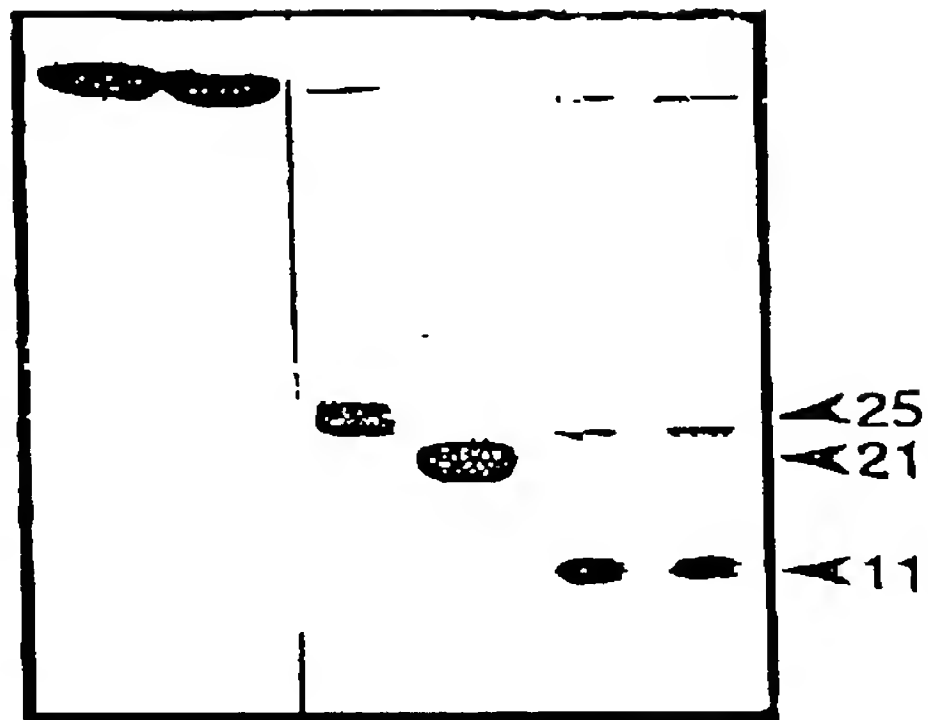


FIGURE 8A

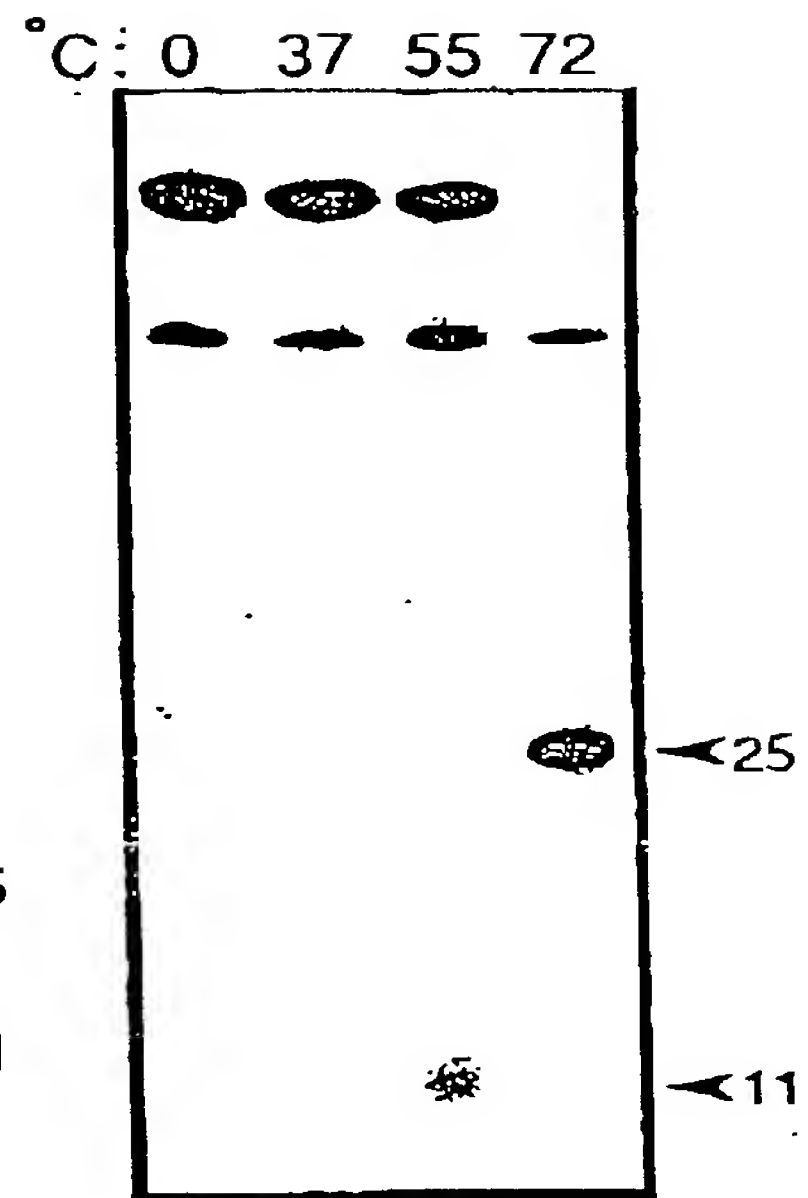


FIGURE 8B

17

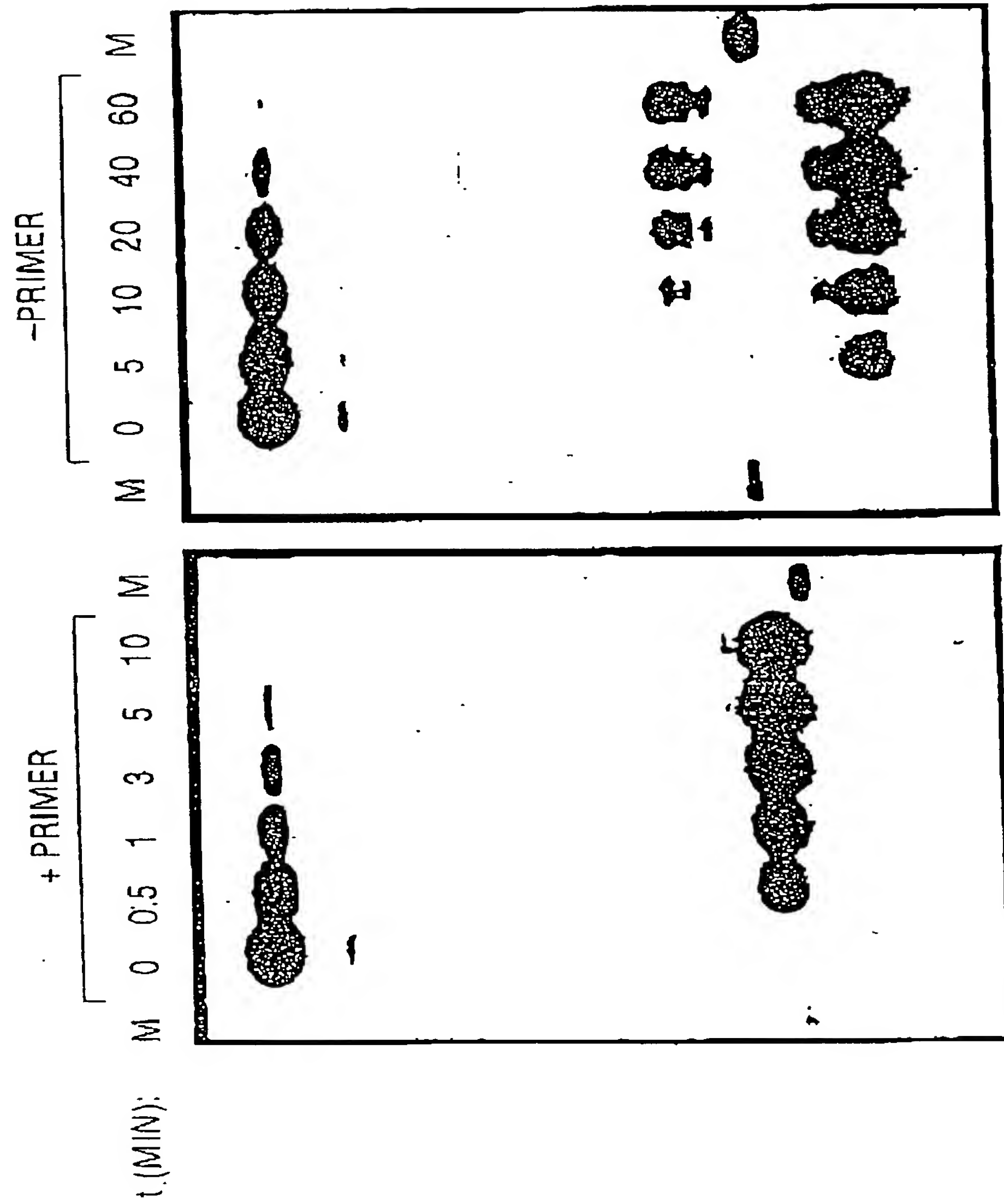


FIGURE 9B

FIGURE 9A

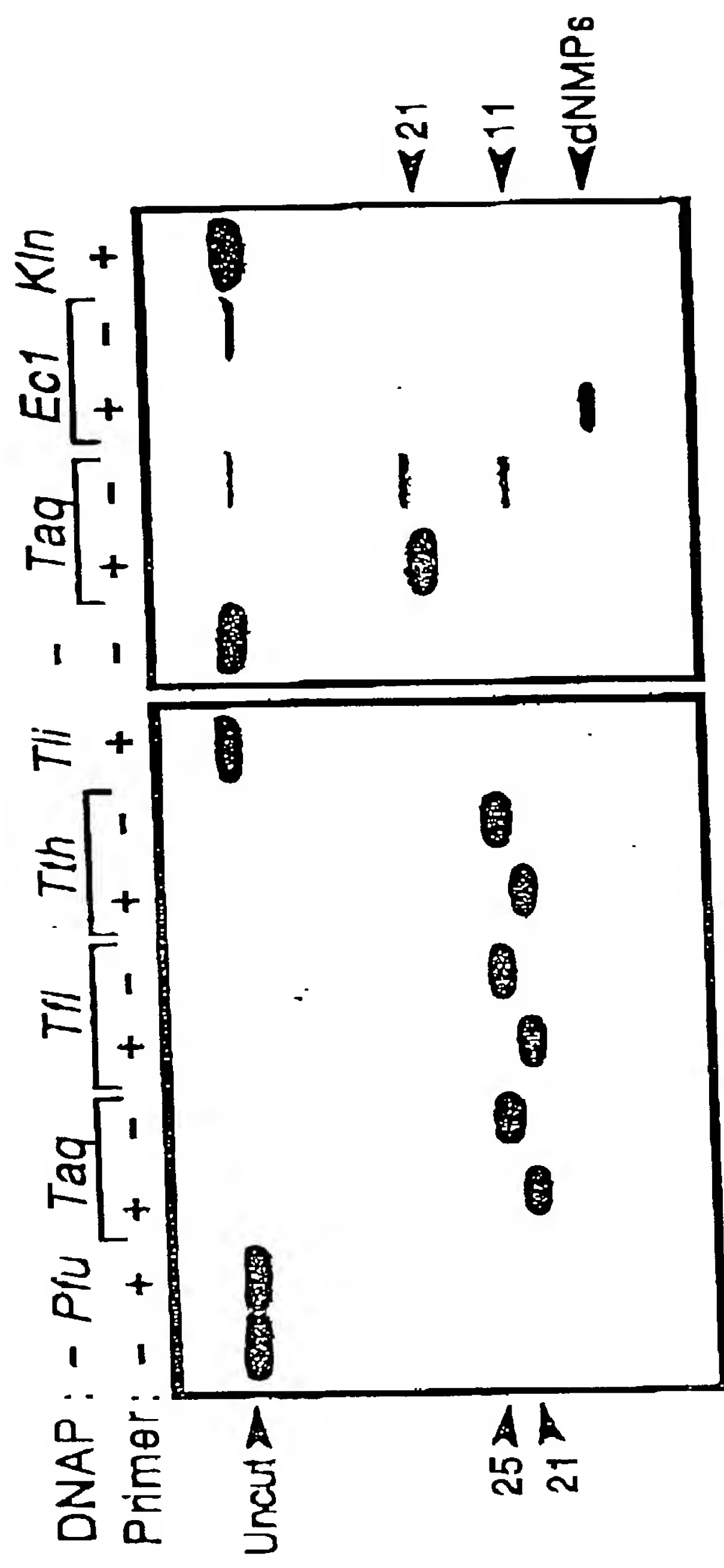
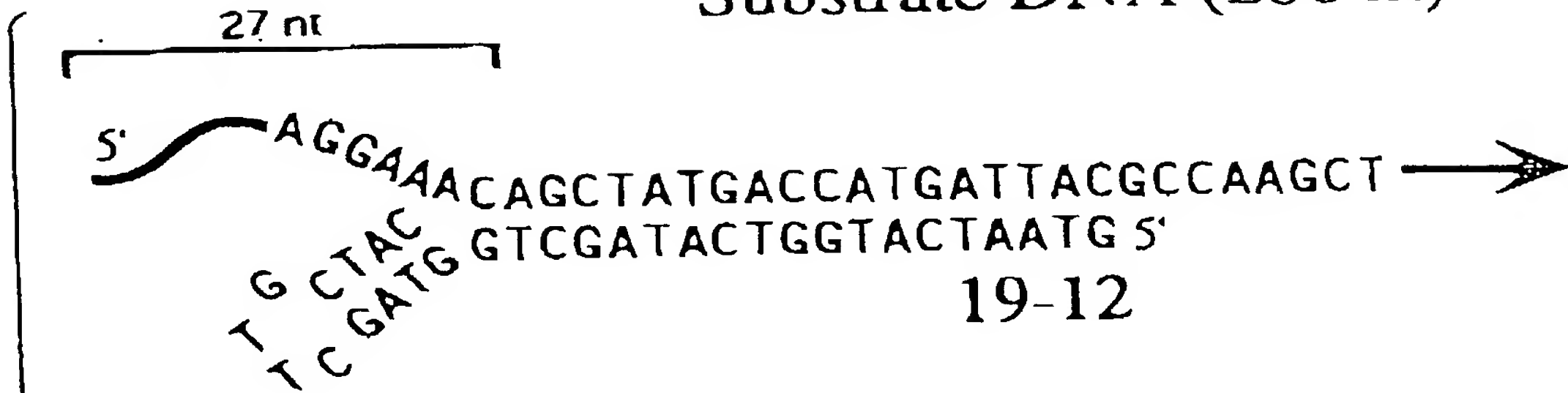


FIGURE 10A

FIGURE 10B

Substrate DNA (206 nt)



Substrate DNA (206 nt)

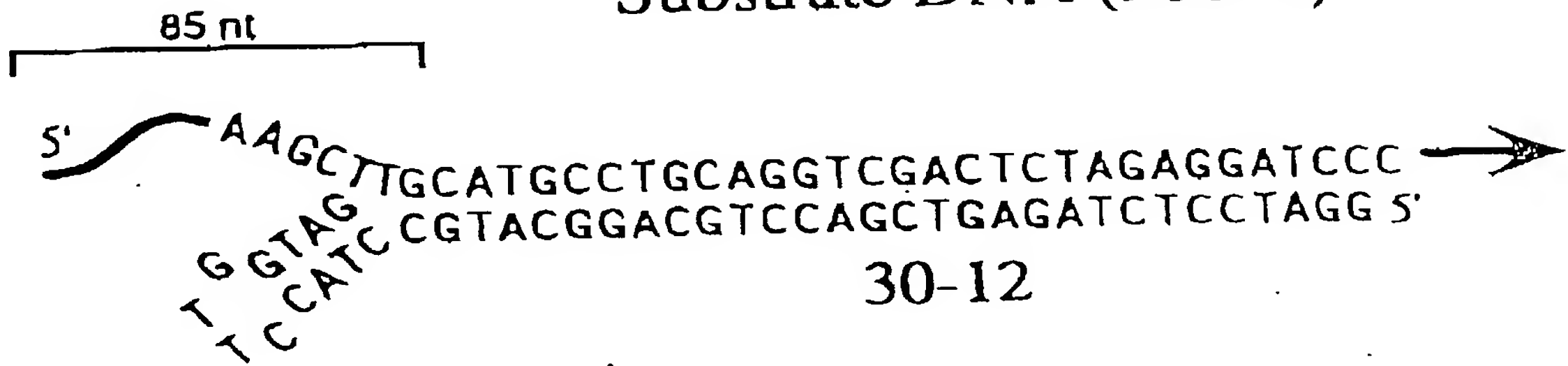


FIGURE 11A

Substrate RNA (46 nt)

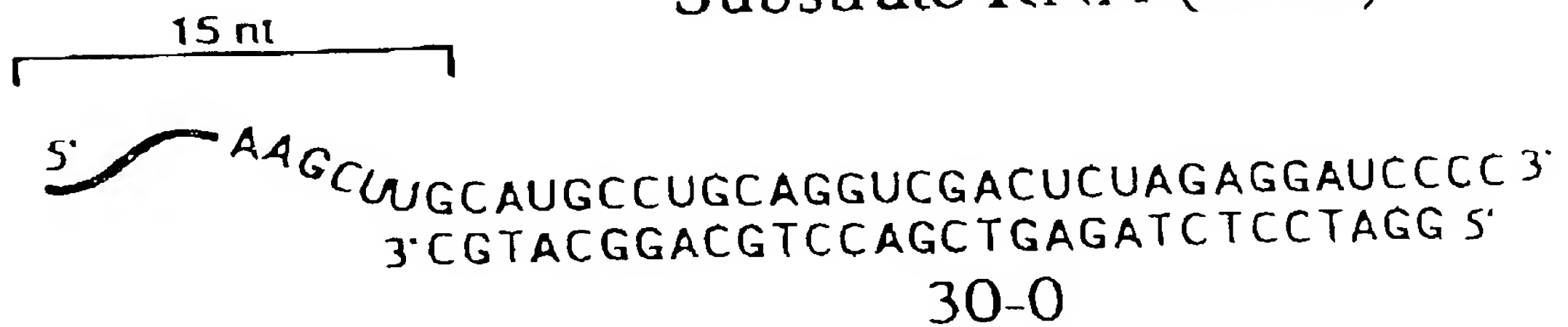


FIGURE 12A

20

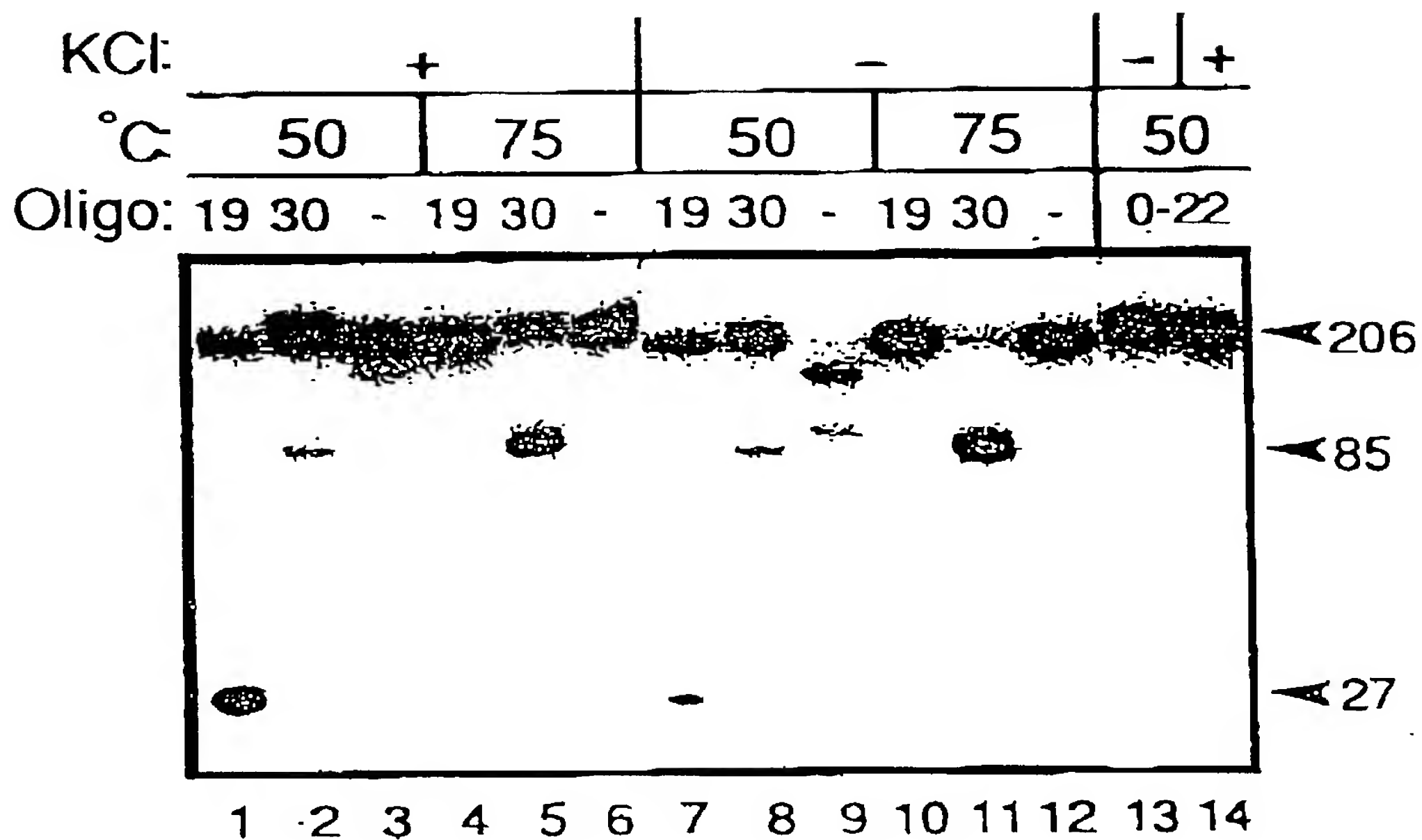


FIGURE 11B

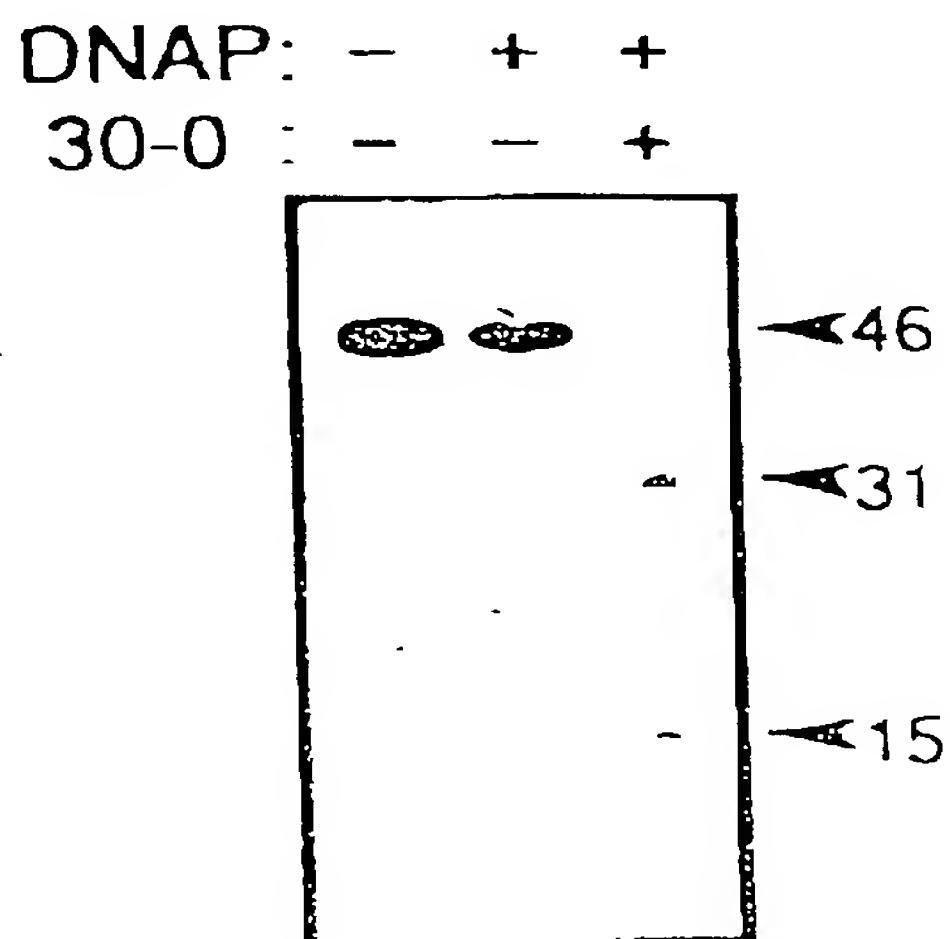
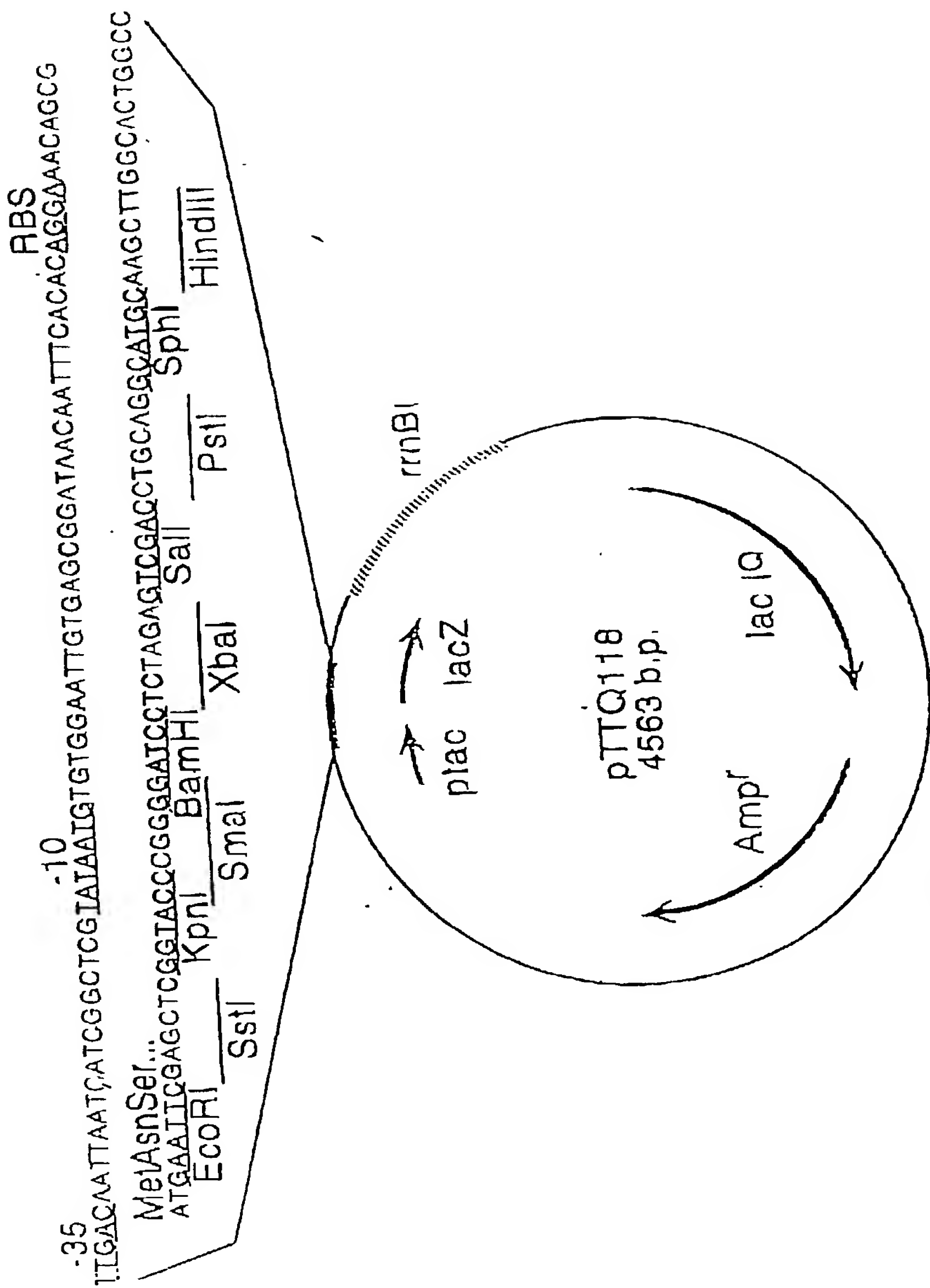


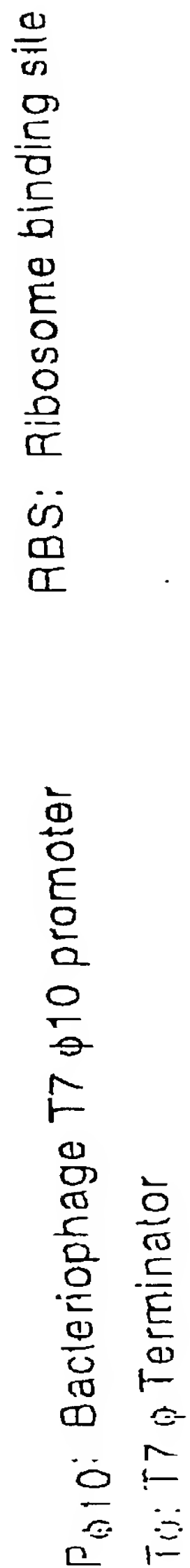
FIGURE 12B

FIGURE 13

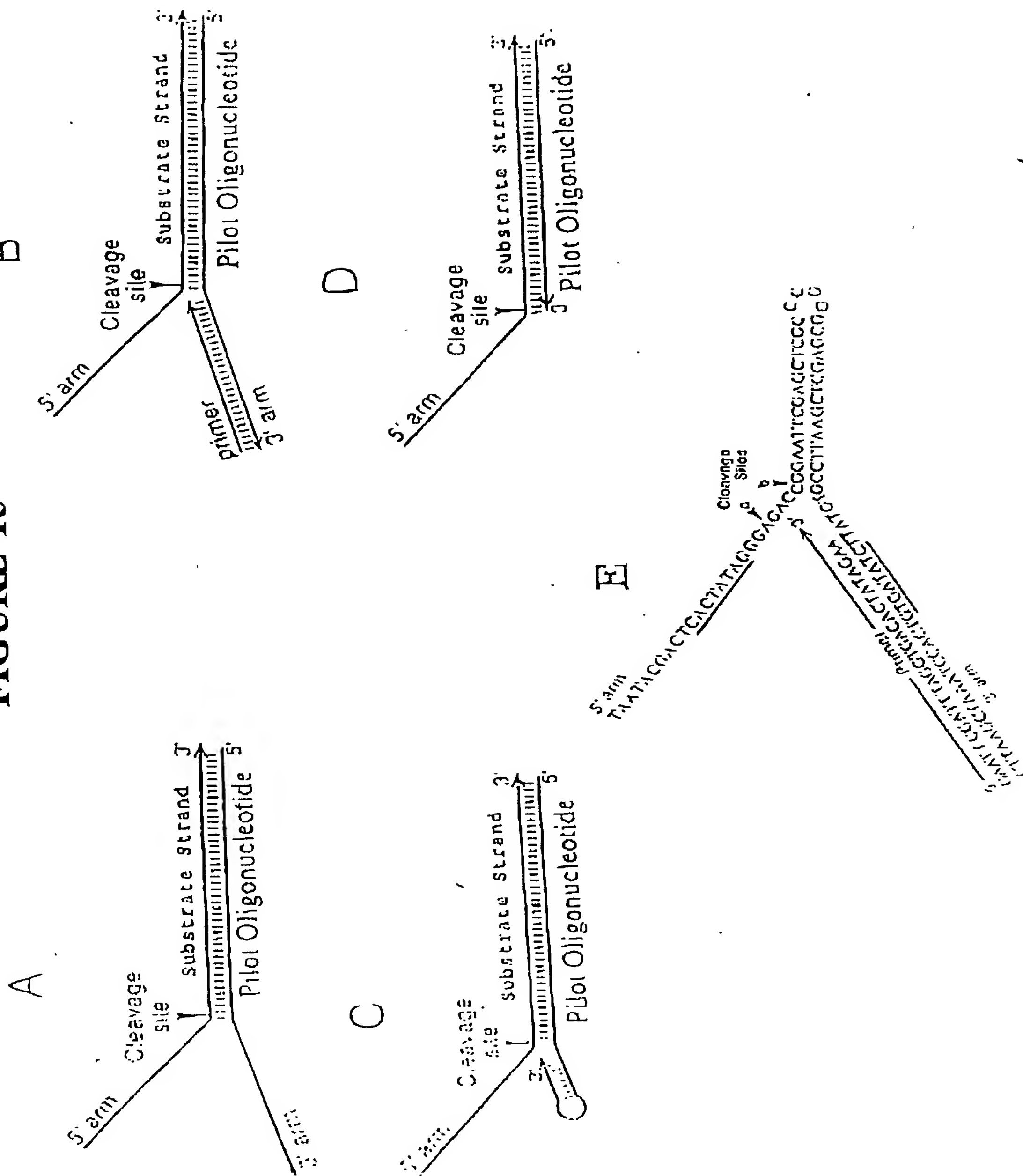


RBS: Ribosome binding site
 lacZ: Beta-galactosidase alpha fragment
 lacI: E. coli lacI repressor gene
 Amp^r: Ampicillin resistance gene
 rrnBI: E. coli rrnB transcription terminator

[REDACTED]



□



111125292 111125292

1 2 3 4 5 6 7

UNCLEAVED SUBSTRATE



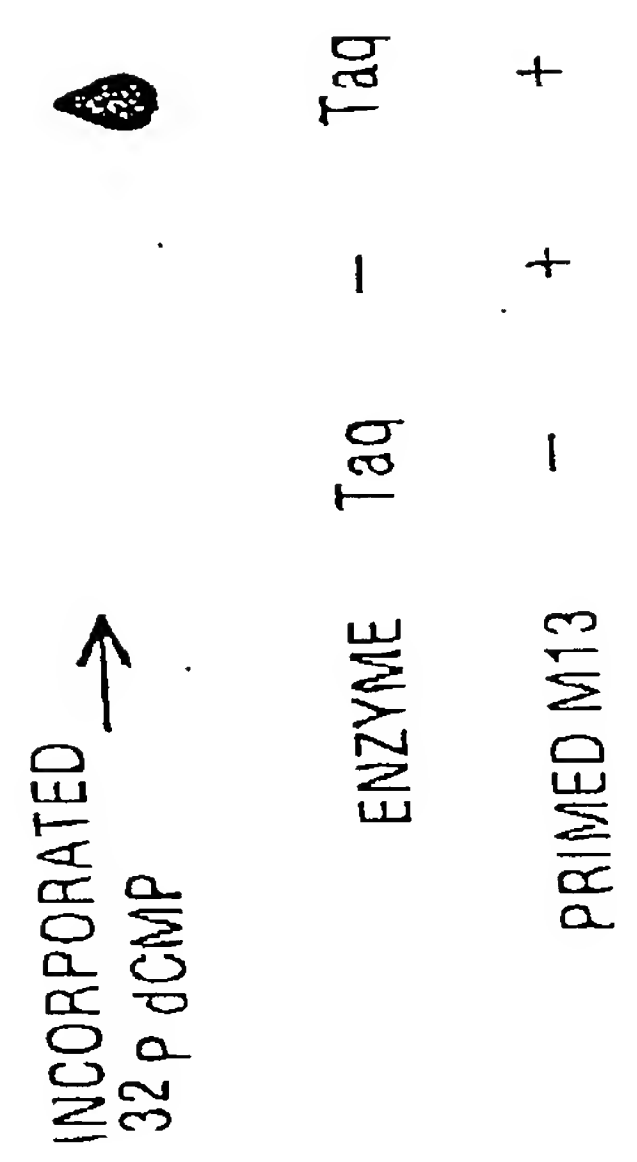
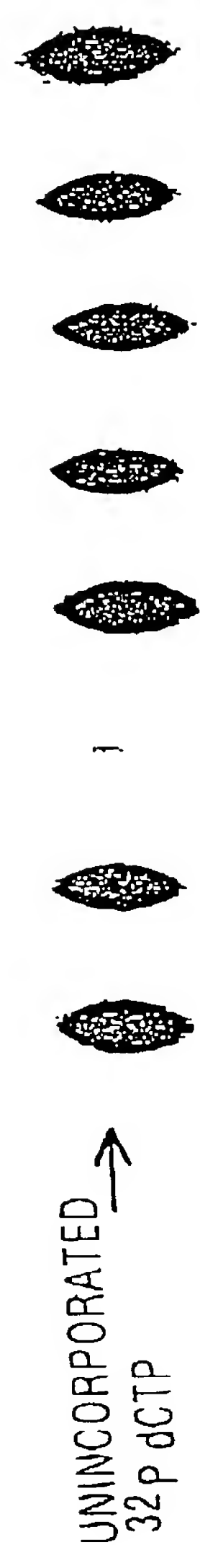
CLEAVED SUBSTRATE



	4e			5b			
Tdq	-	-	+	-	-	+	dNTPs
	-	-	+	-	-	+	PRIMER
							ENZYME

FIGURE 16

25



ENZYME	Taq	-	Taq	4b	4c	4d	4e	4f
PRIMED M13	-	+	+	+	+	+	+	+

FIGURE 17

22

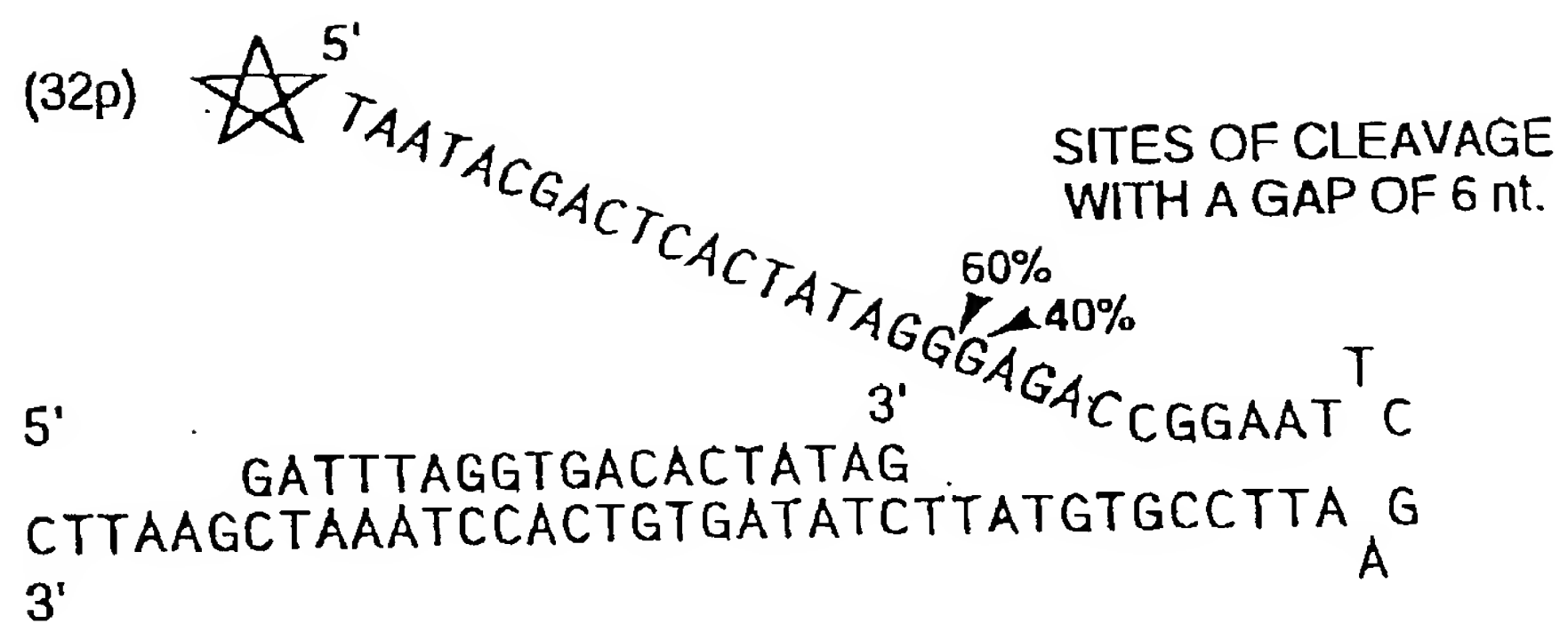
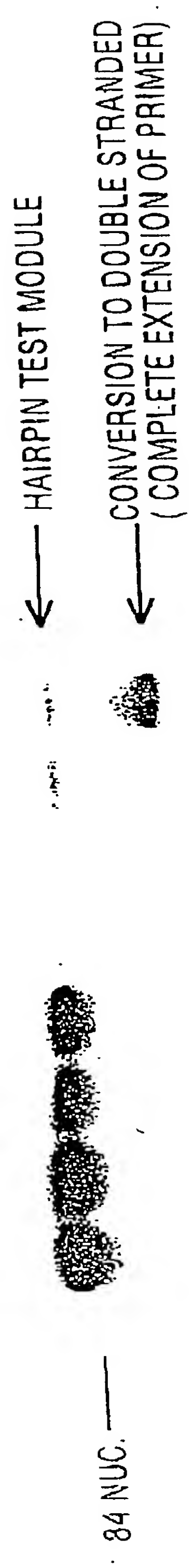


FIGURE 18A

		"4d"		"4b"		UNMODIFIED	
		NO POL. ACTIVITY		2 PT. MUTATION SMALL ACTIVITY		DNAP Taq	
1	2	3	4	5	6	7	8
-	-	-	+	-	+	-	+
						dNTP	



DESIRED
PRODUCT
21 NUC. →

↑ SOME ABERRANT CLEAVAGE WITH "4b"
BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

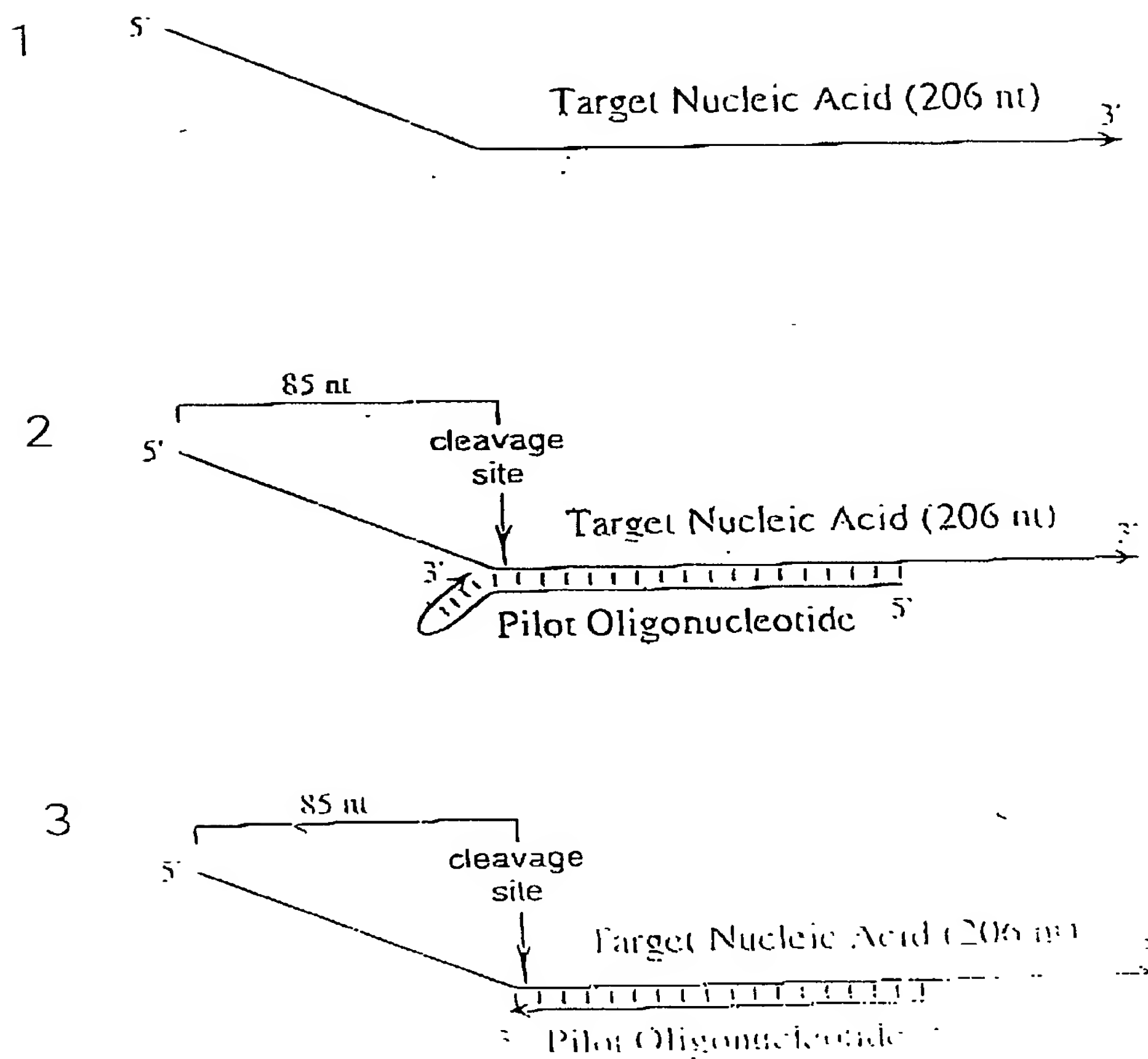
FIGURE 18B

[illegible]

220

29

FIGURE 20A



30

[REDACTED]

I II III IV V VI
1 1 2 3 1 1 2 3 1 1 2 3 1 1 2 3 1 1 2 3

—206

206 —

—85

85 —

FIGURE 20B

[REDACTED]

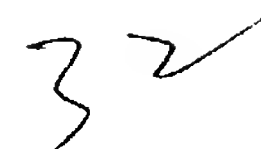


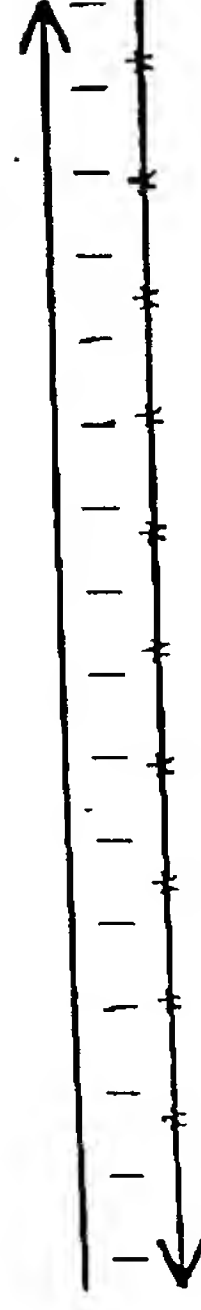
FIGURE 21A

FIGURE 22A



— 206

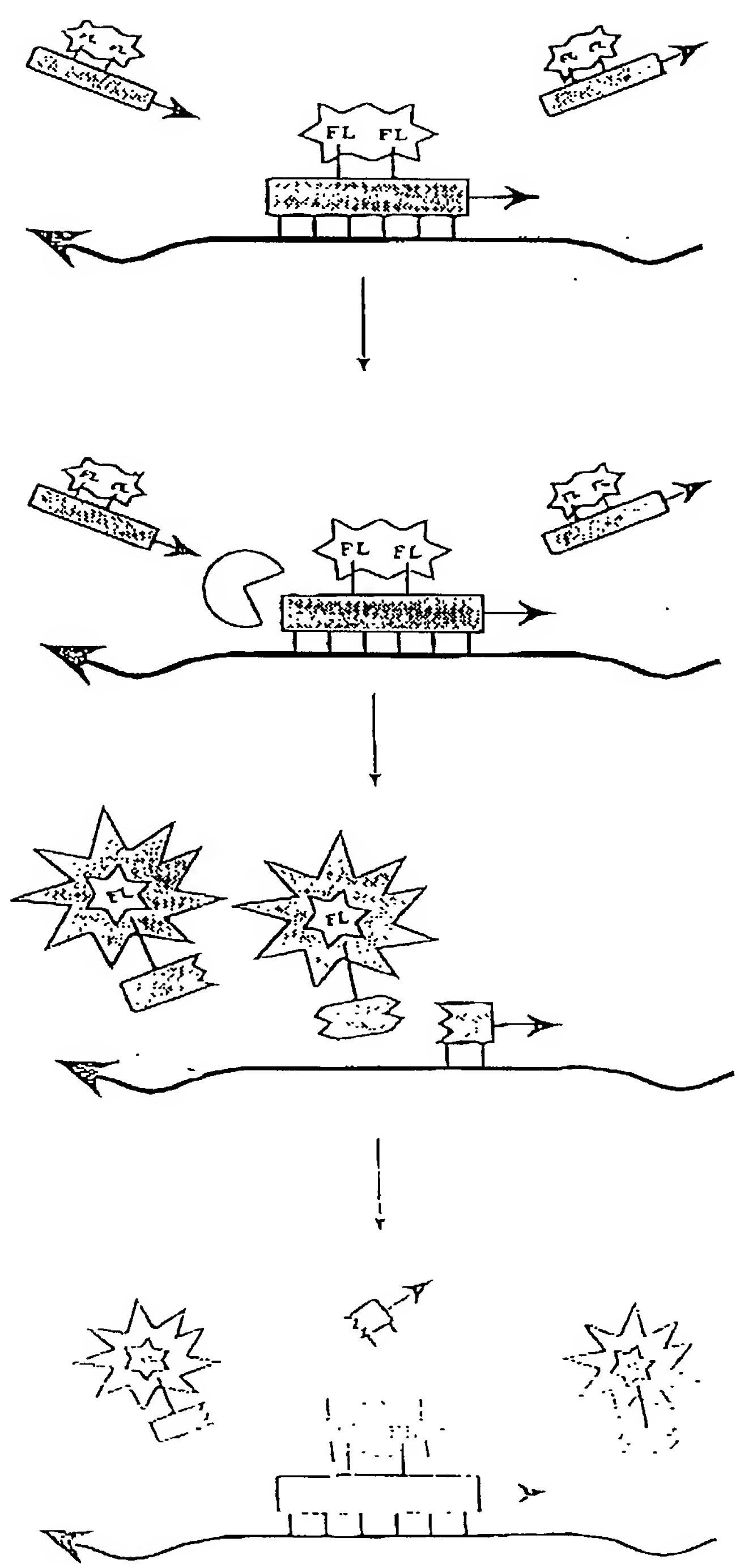
FIGURE 22B



* = 32p

33

FIGURE 23



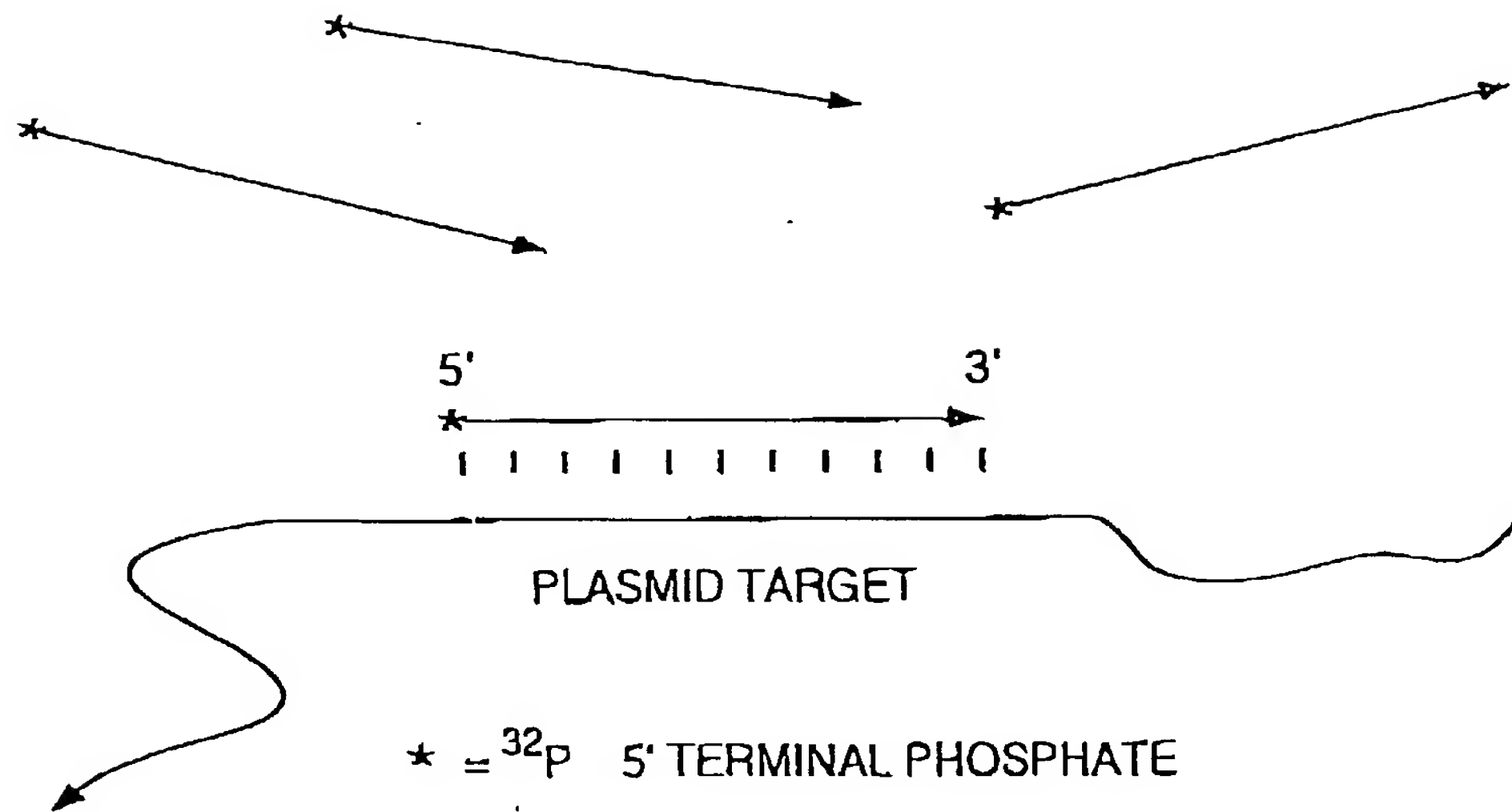


FIGURE 24A

[illegible]

M	1	2	3	4	5	6
---	---	---	---	---	---	---

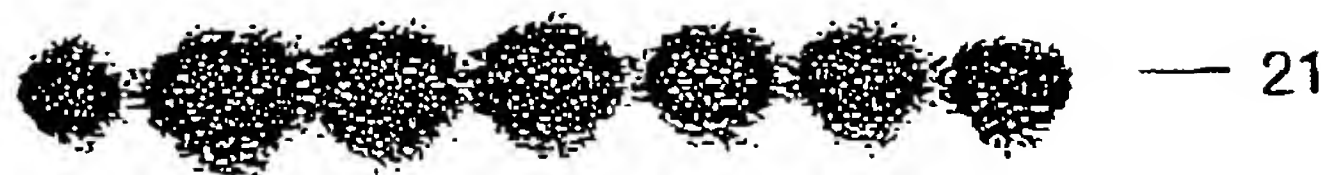
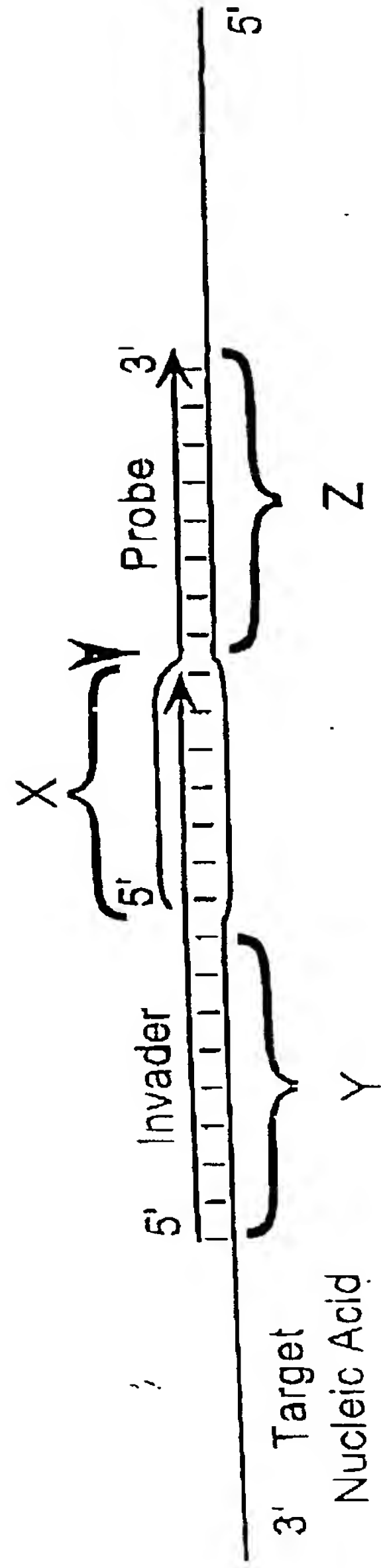


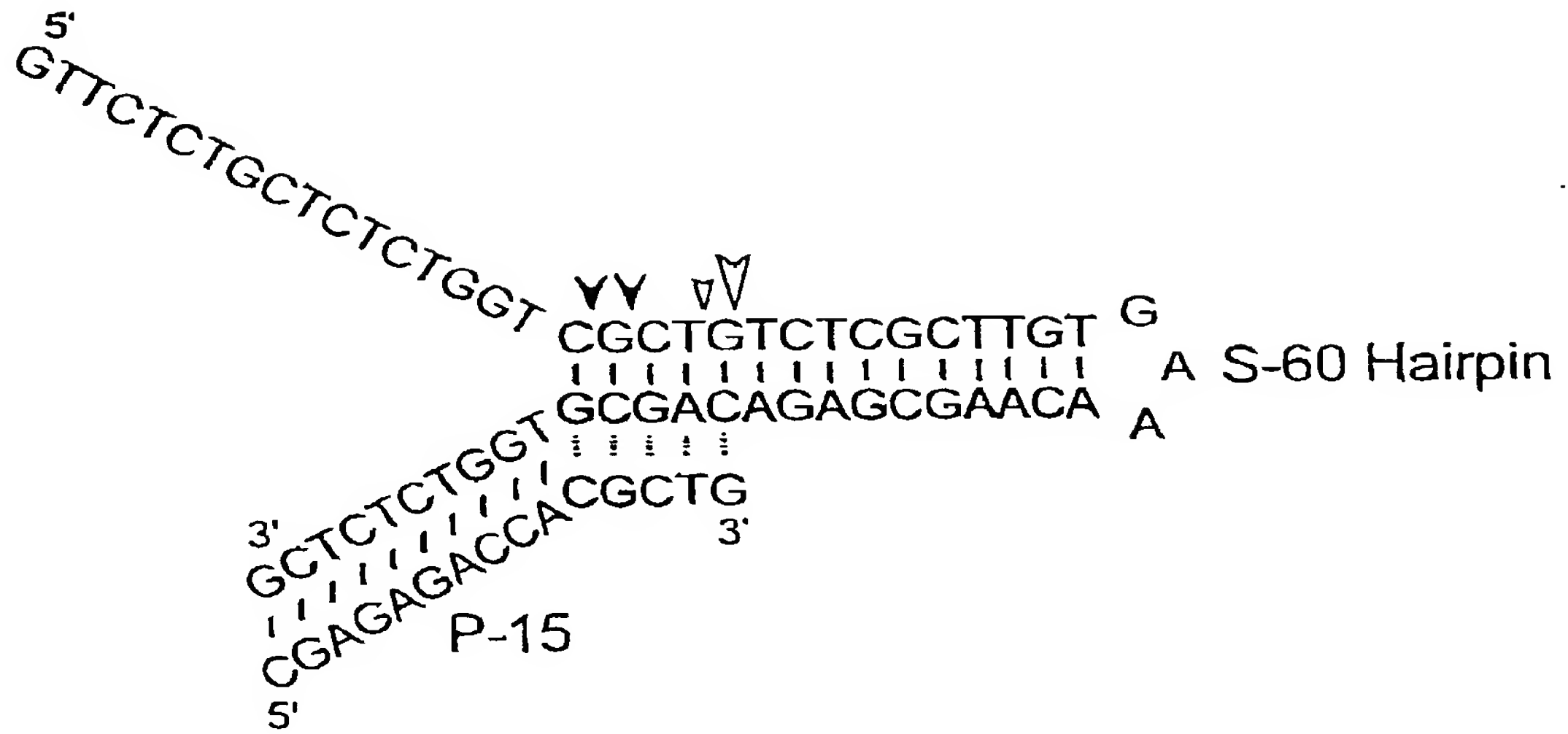
FIGURE 24B

FIGURE 25



22

FIGURE 26



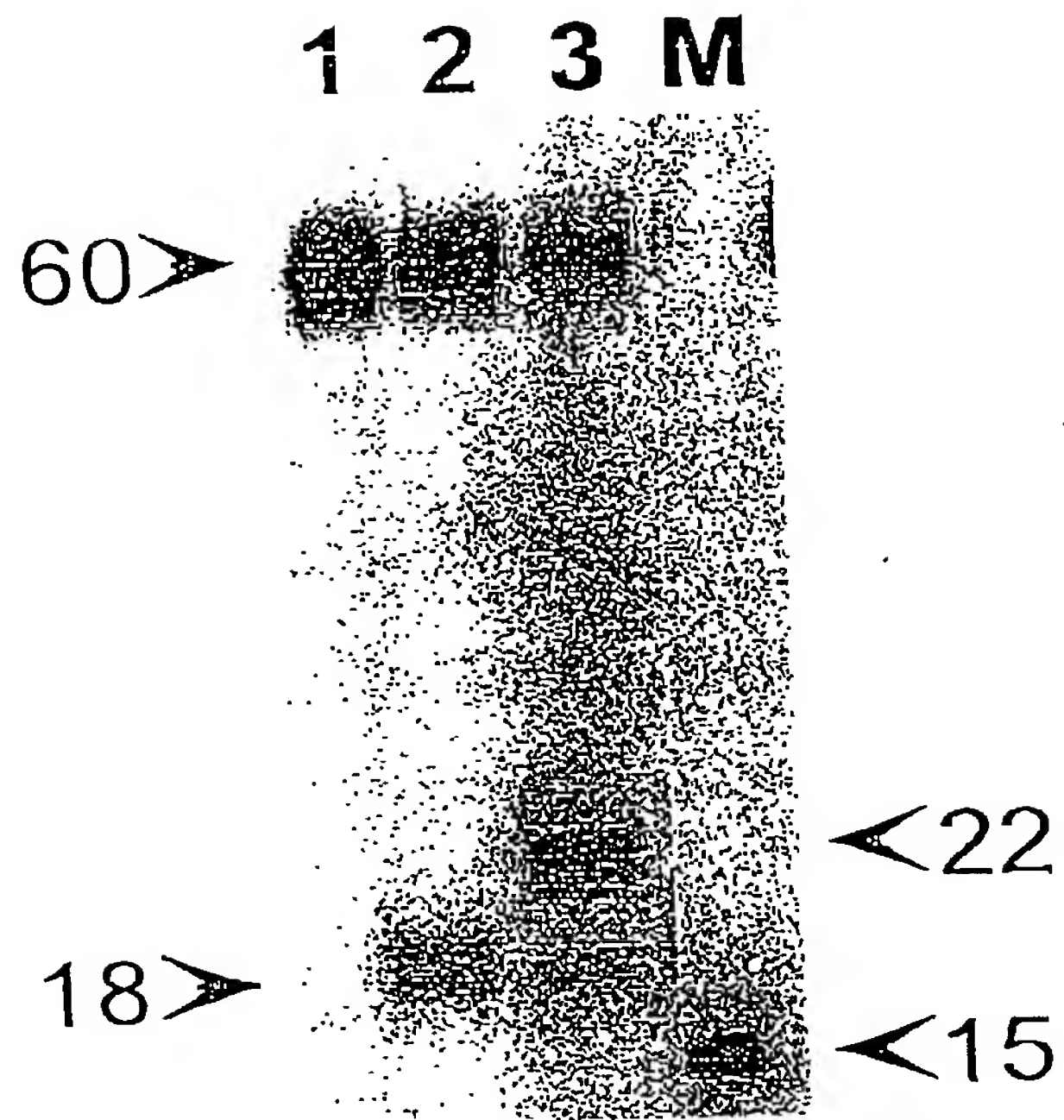


FIGURE 27

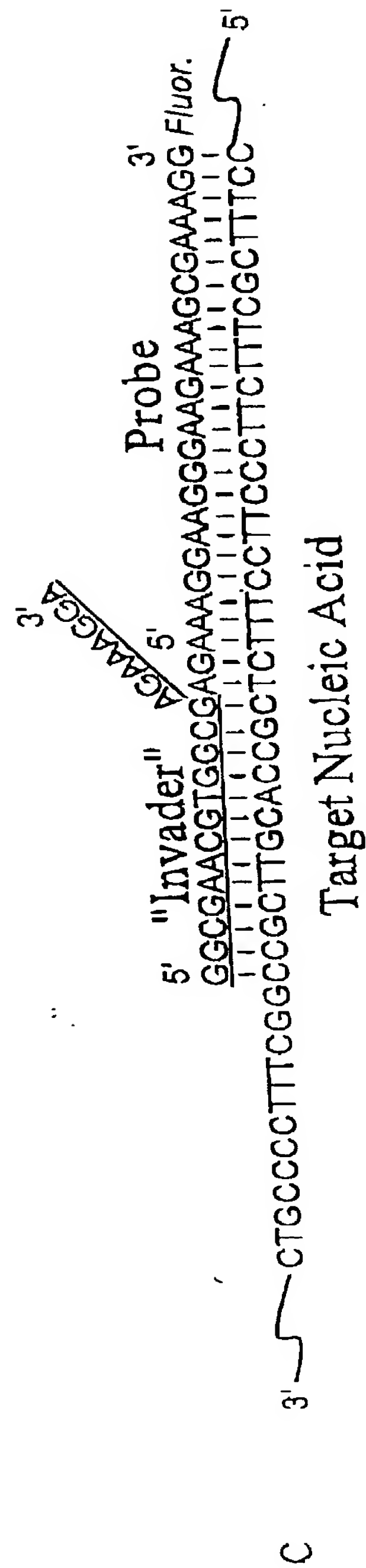
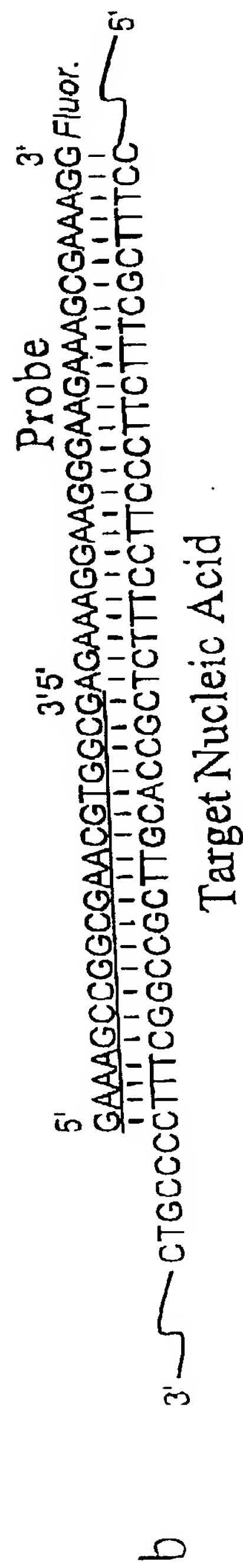
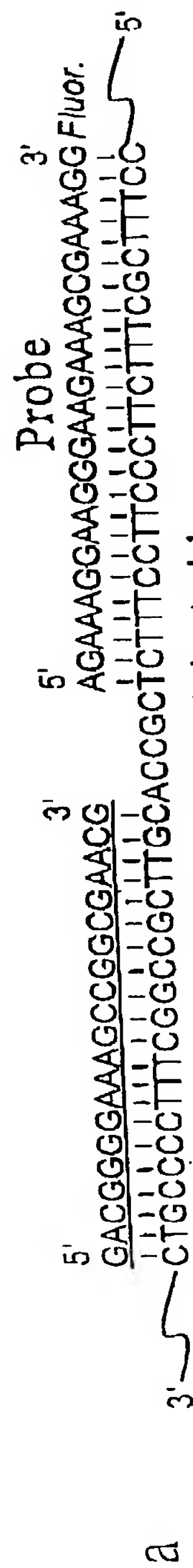
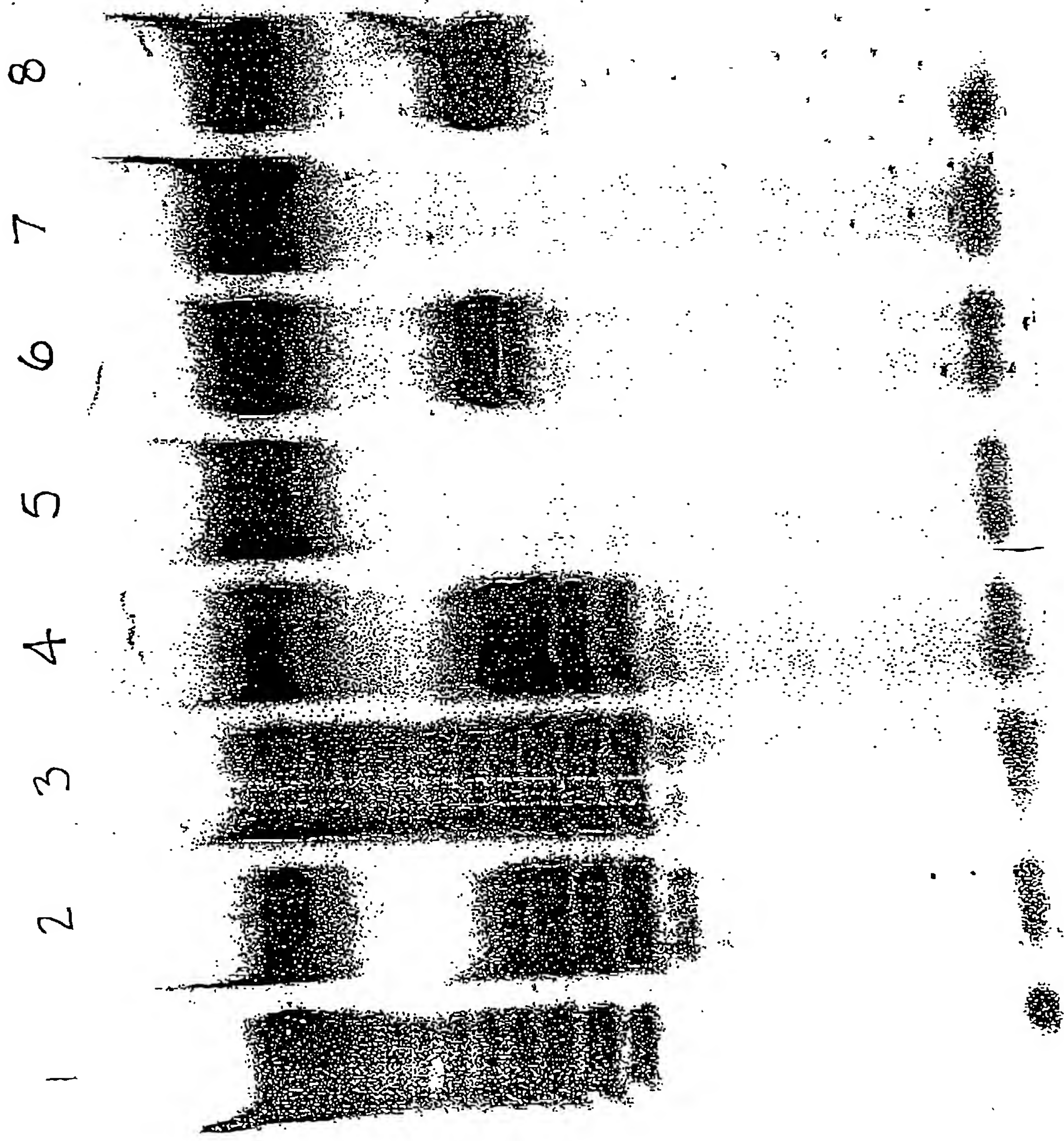


FIGURE 29



267

4.1

FIGURE 30

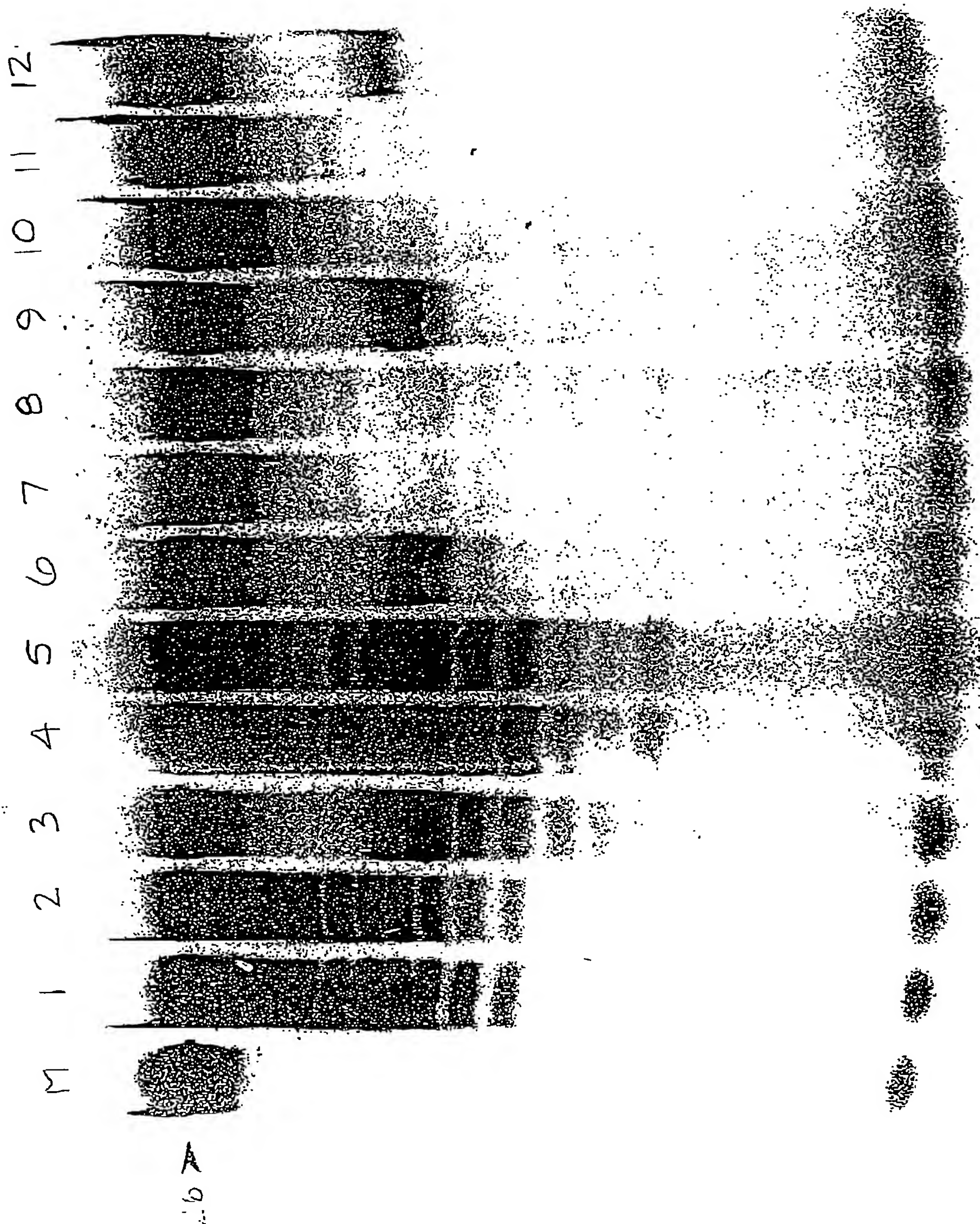
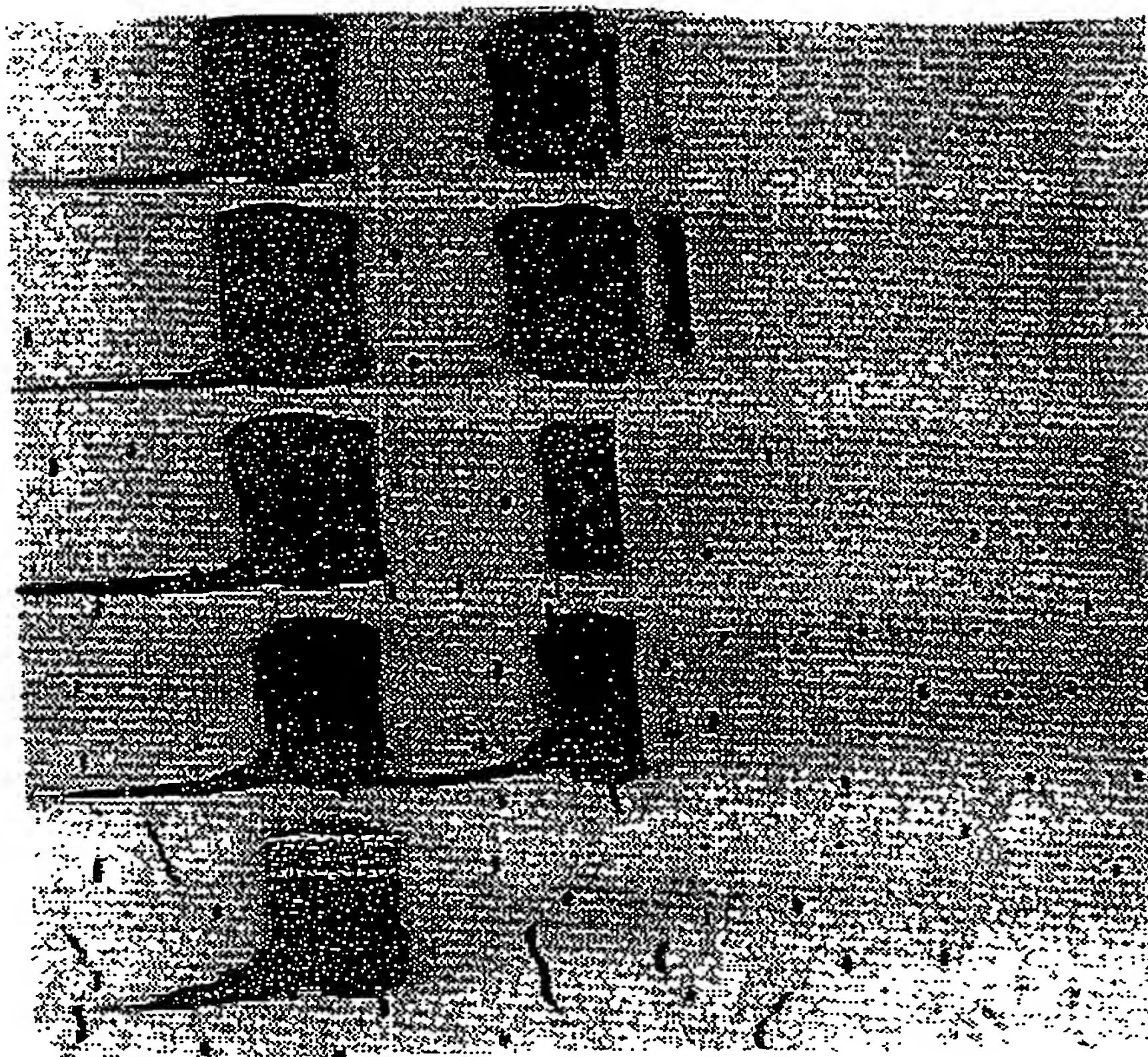


FIGURE 3

1 2 3 4 5



26

43

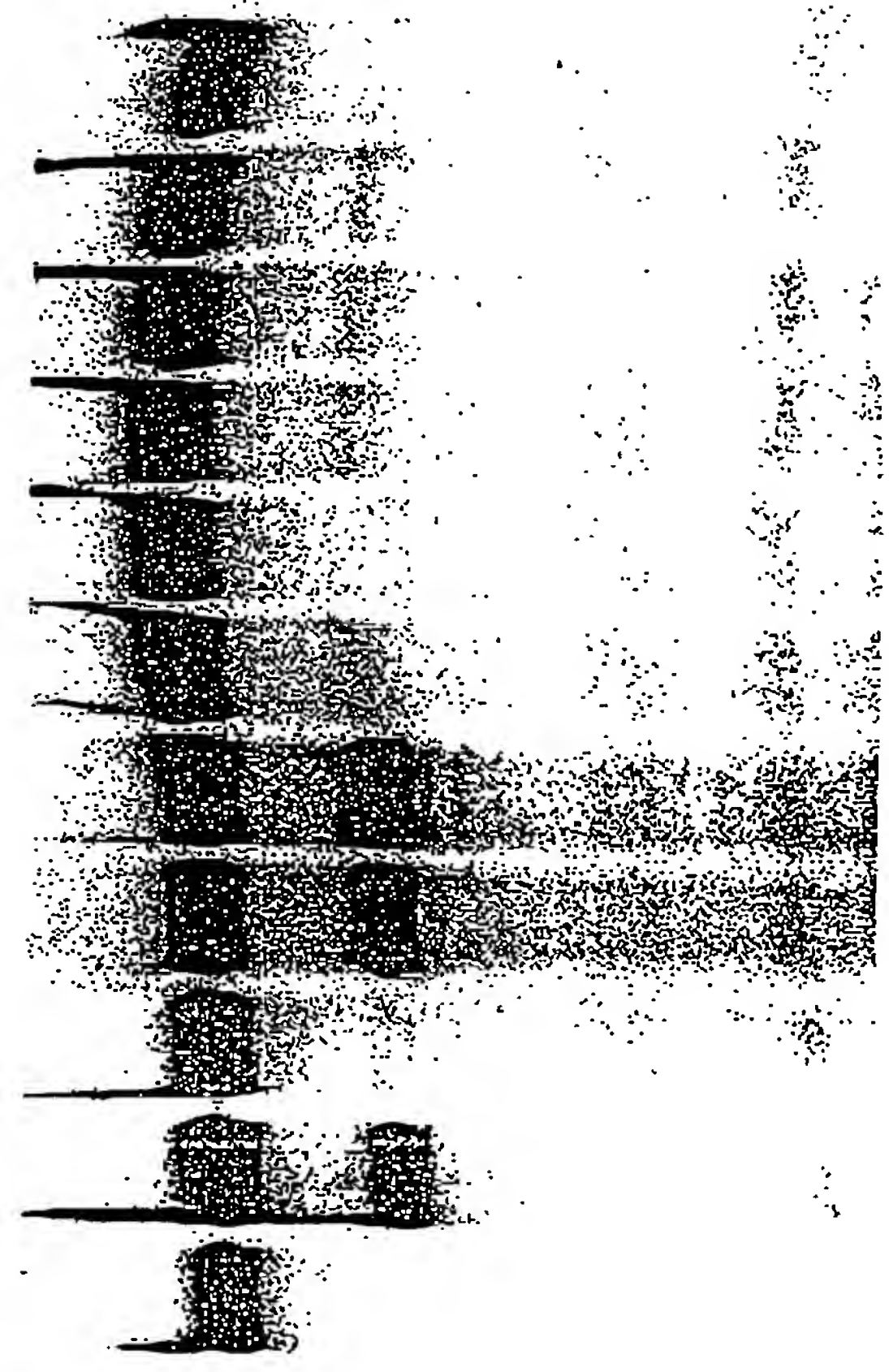
[REDACTED]



[Redacted]

FIGURE 33

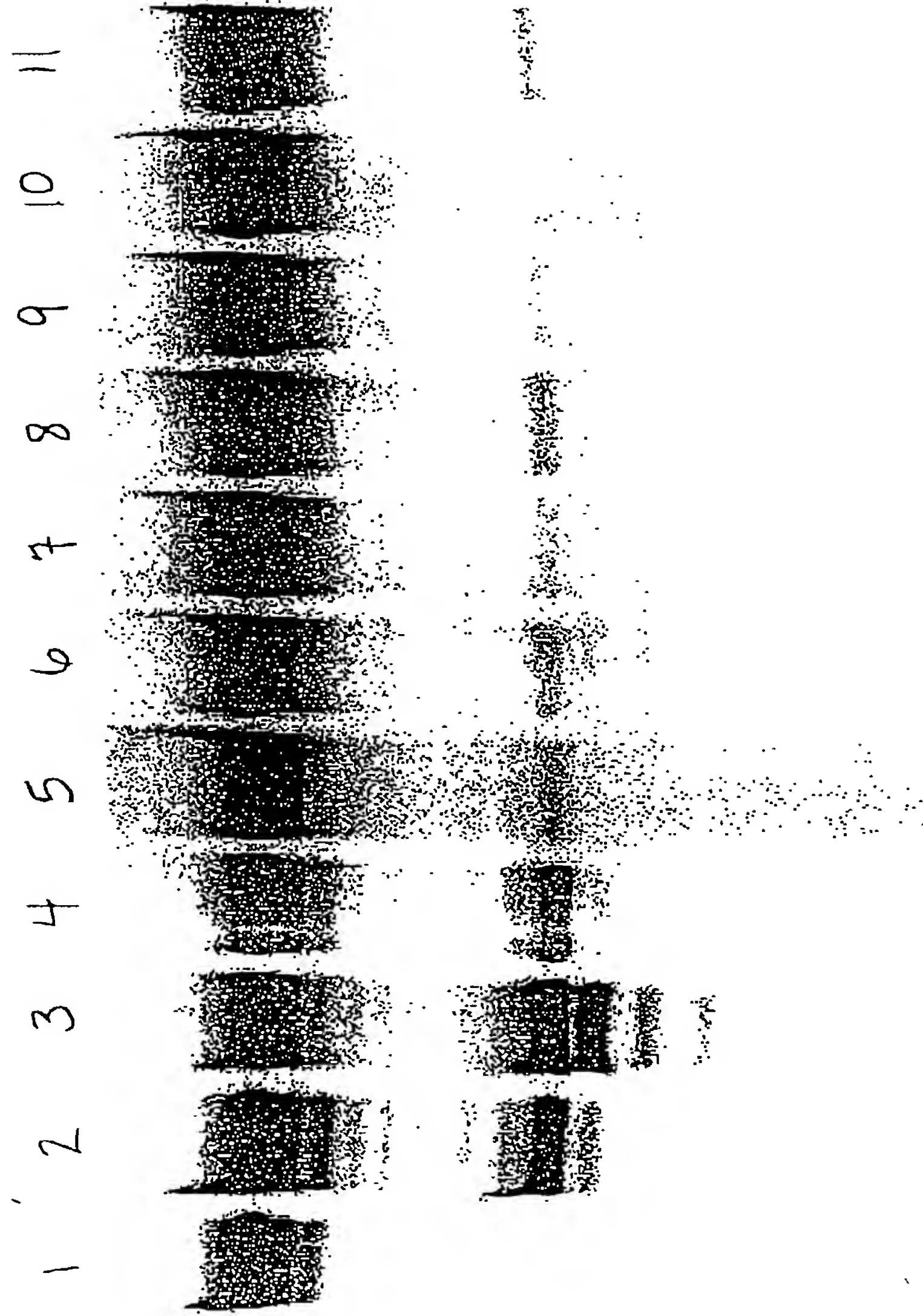
1 2 3 4 5 6 7 8 9 10 11



A A

45

FIGURE 34



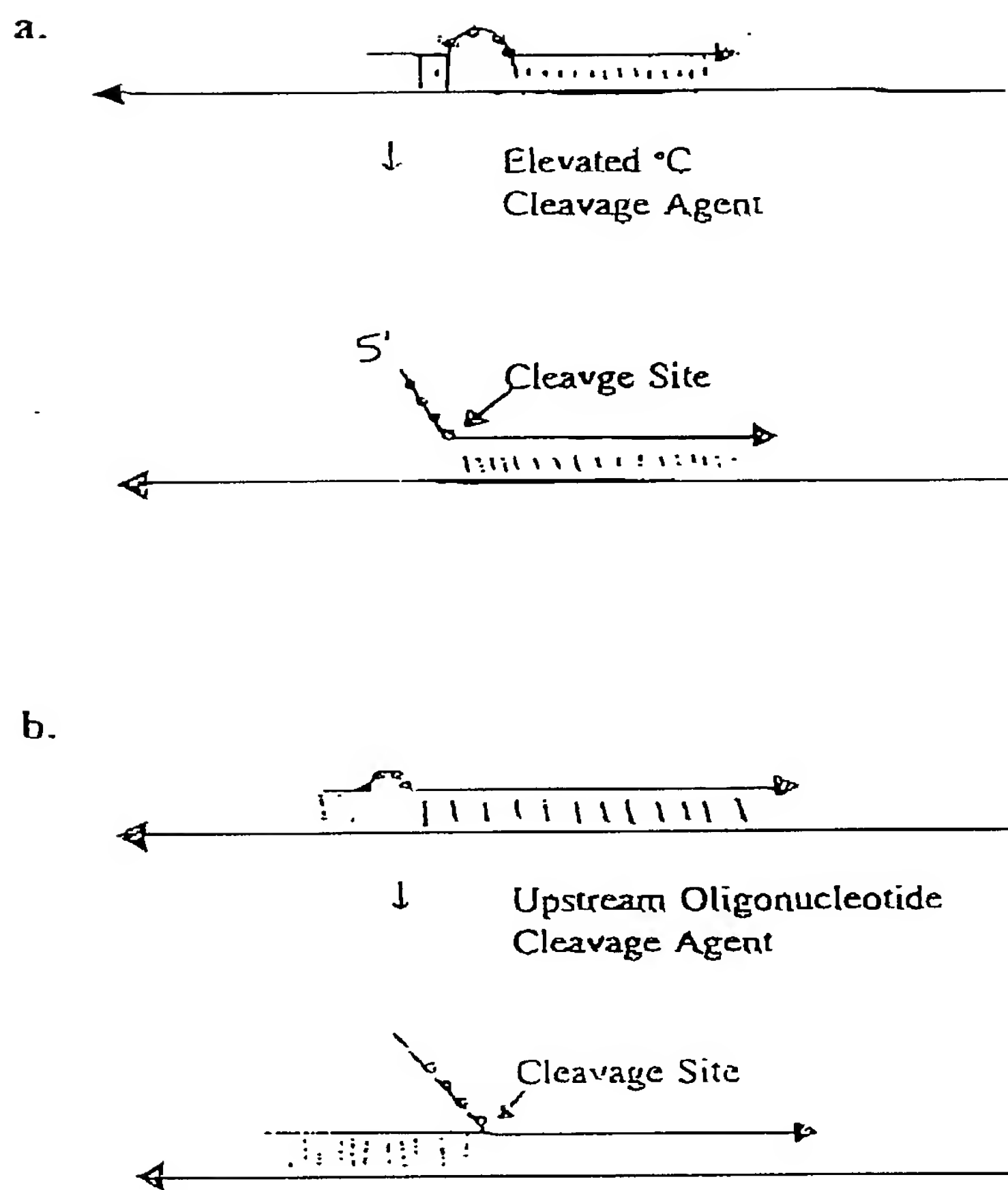


FIGURE 36

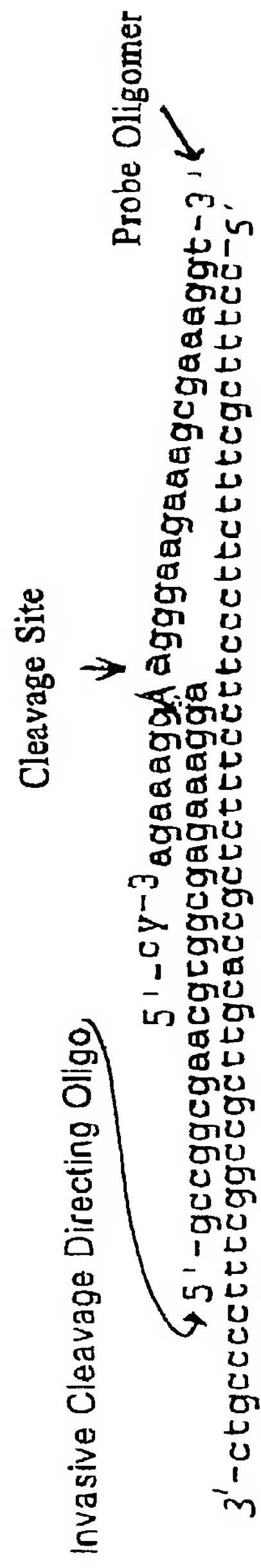


FIGURE 37

FIGURE 38

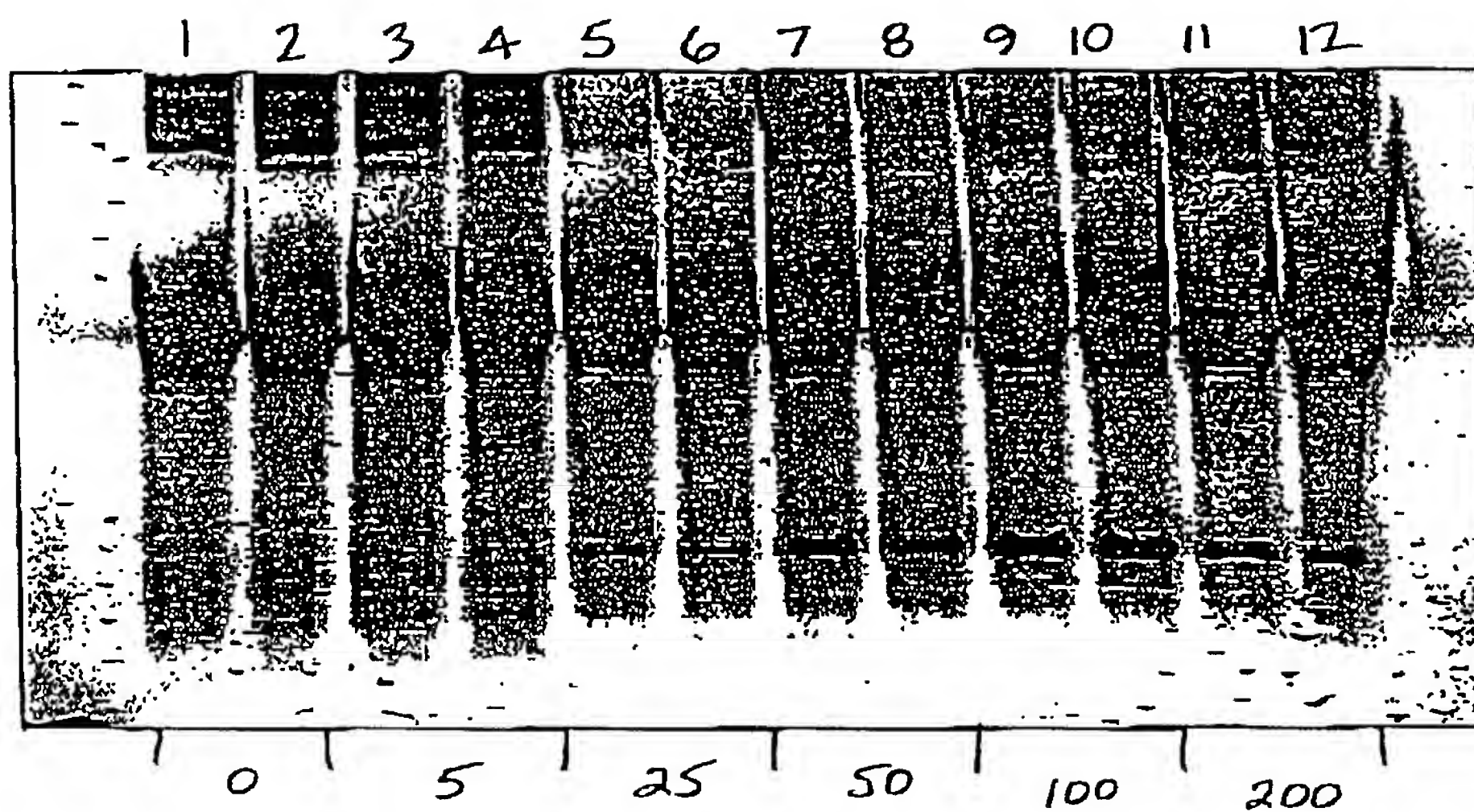
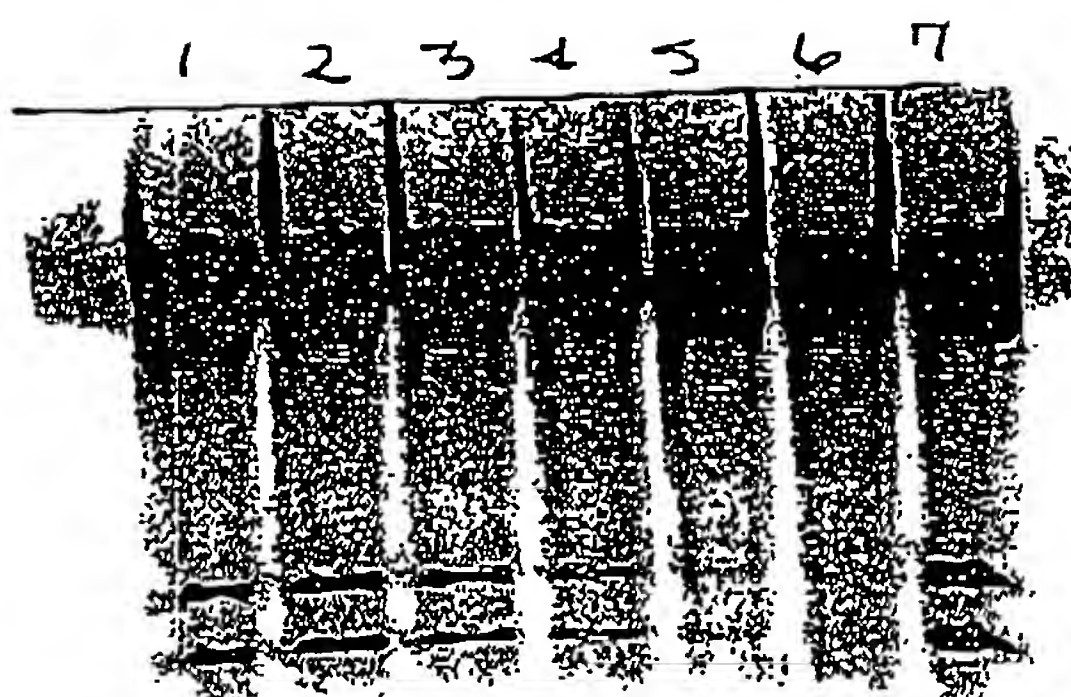


FIGURE 40



52





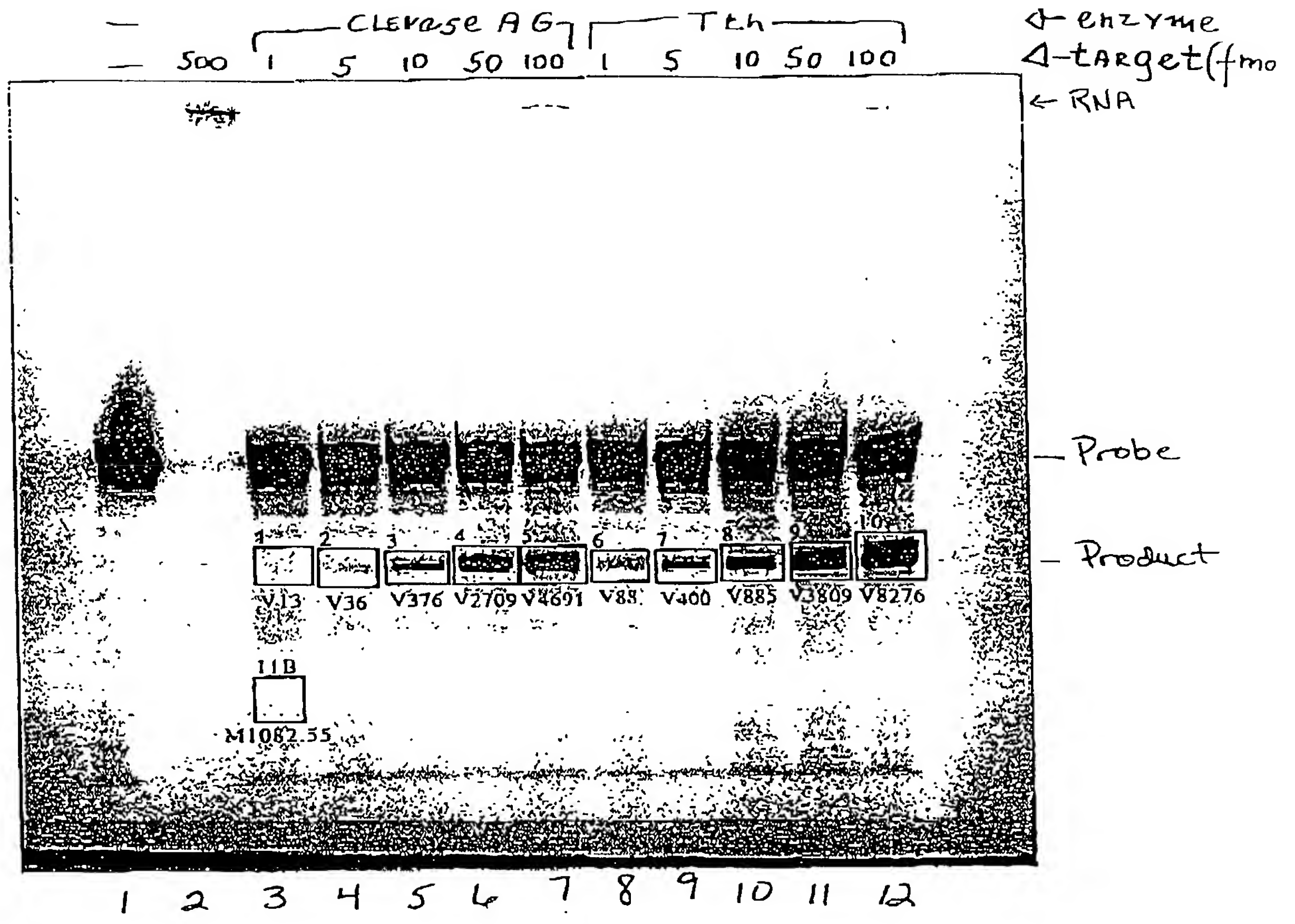


FIGURE 43

SS

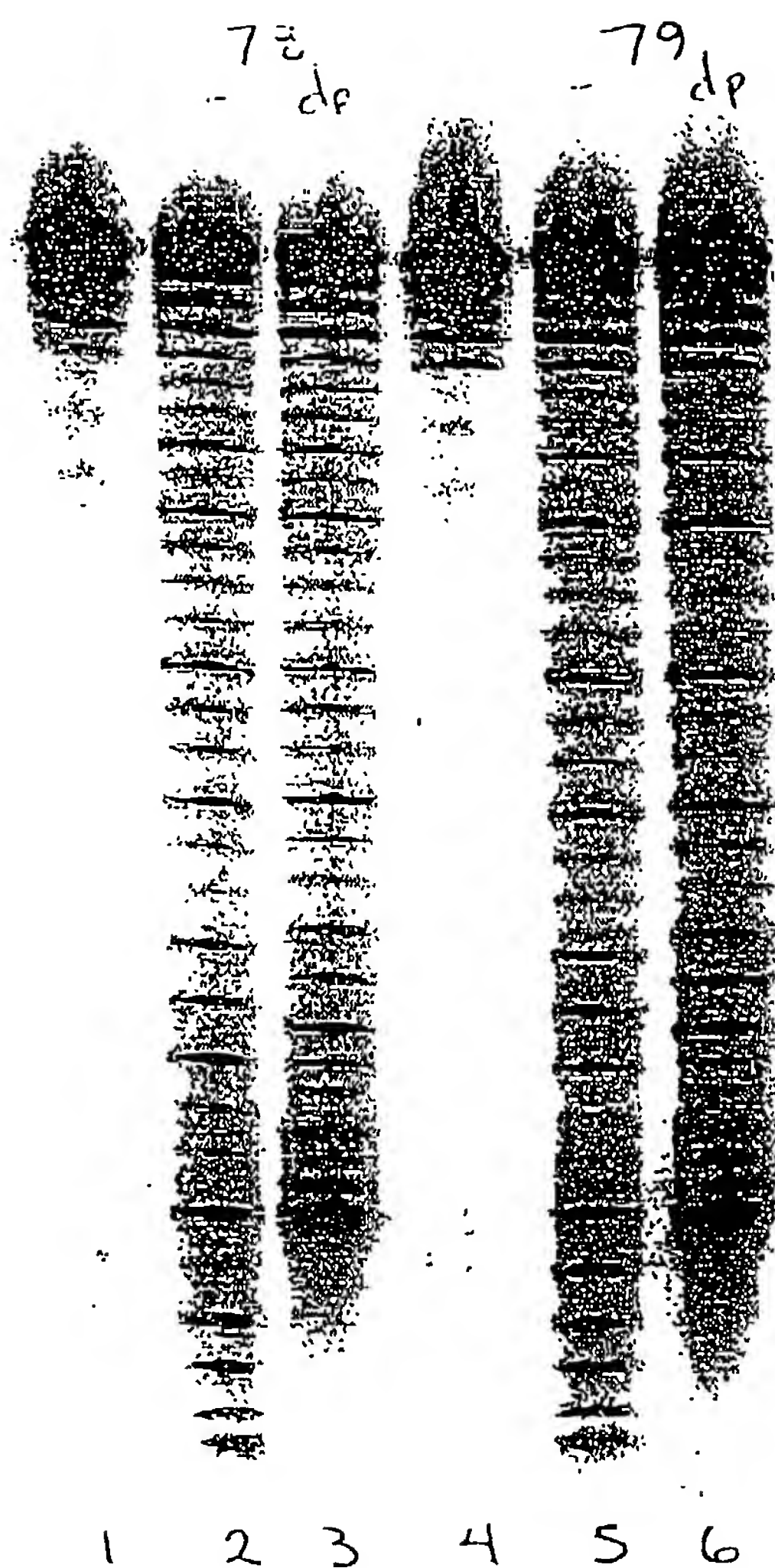
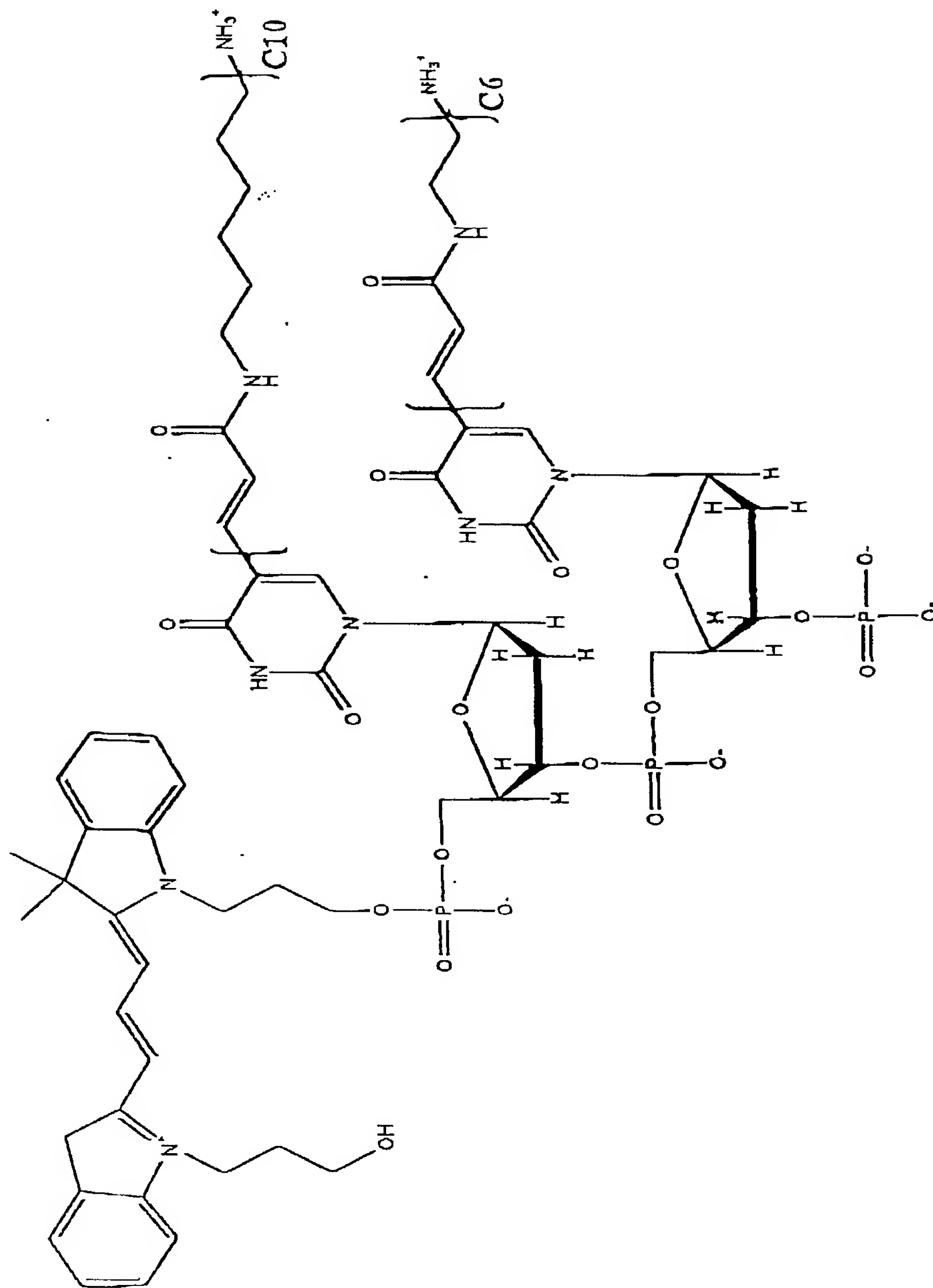


FIGURE 44

FIGURE 45

70 (C10 aminoT's)

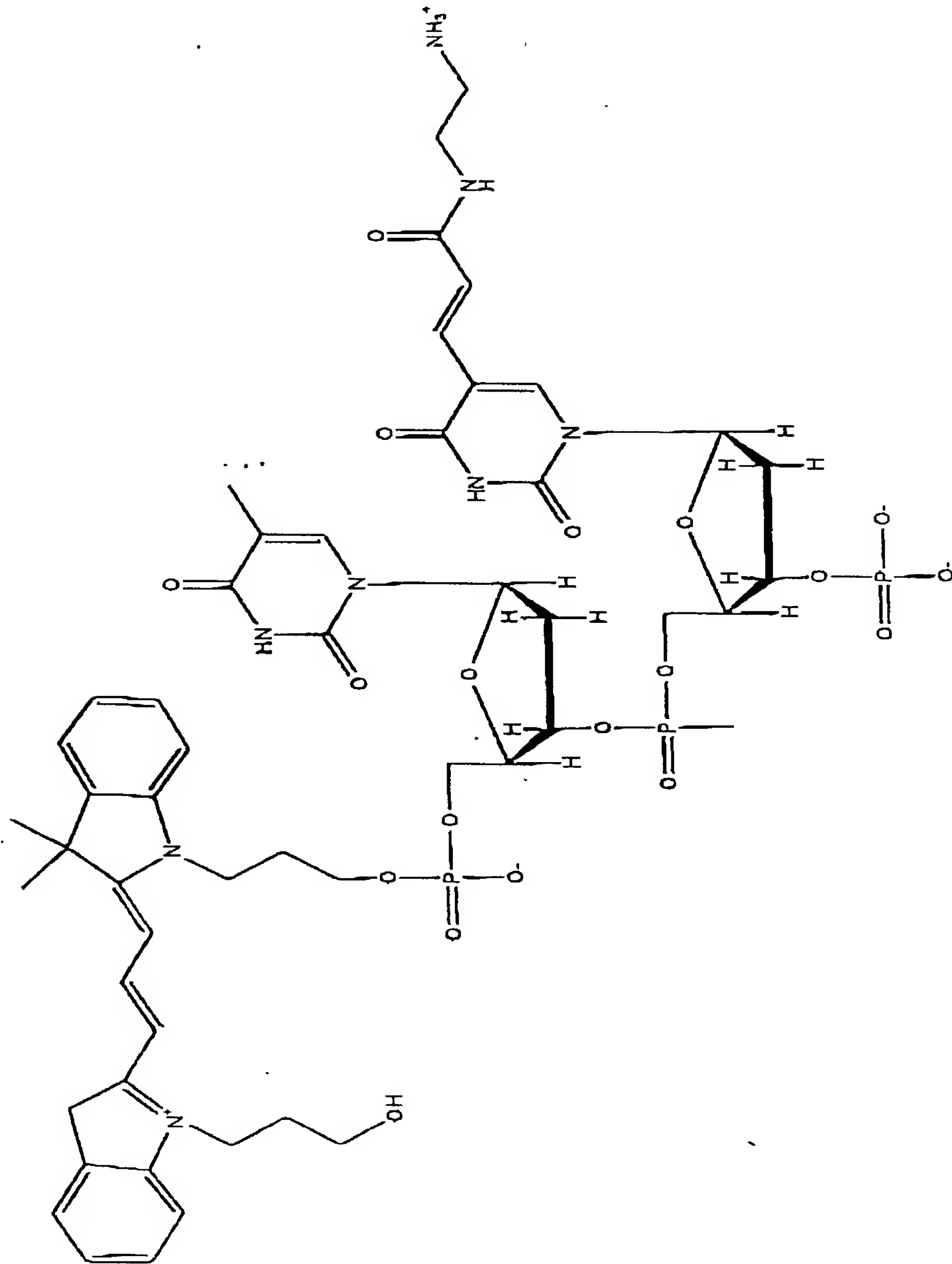
74 (C6 amino T's)



57

FIGURE 46

75

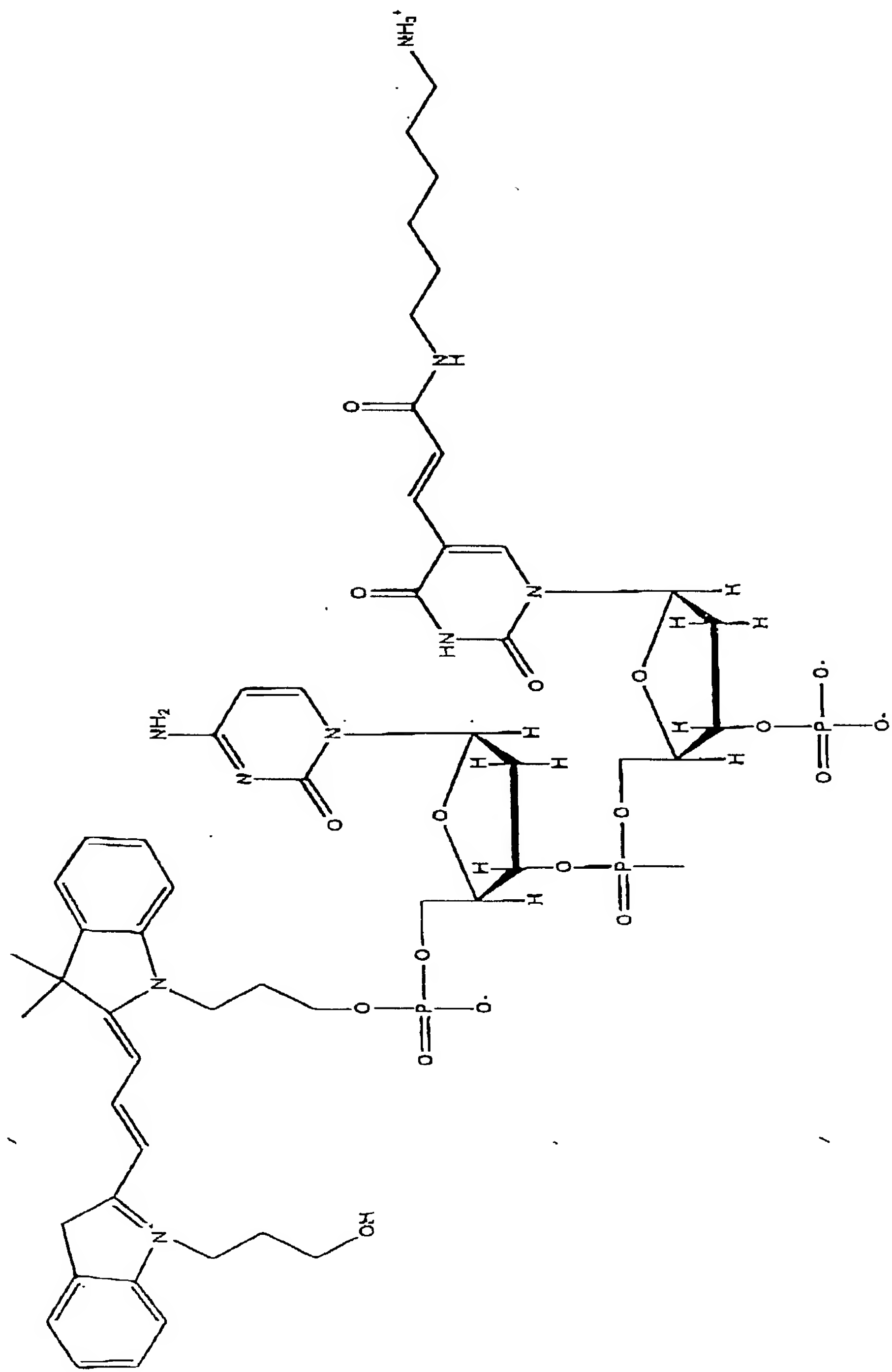


58

12-11-83 11:54 AM

FIGURE 47

76



59

FIGURE 48

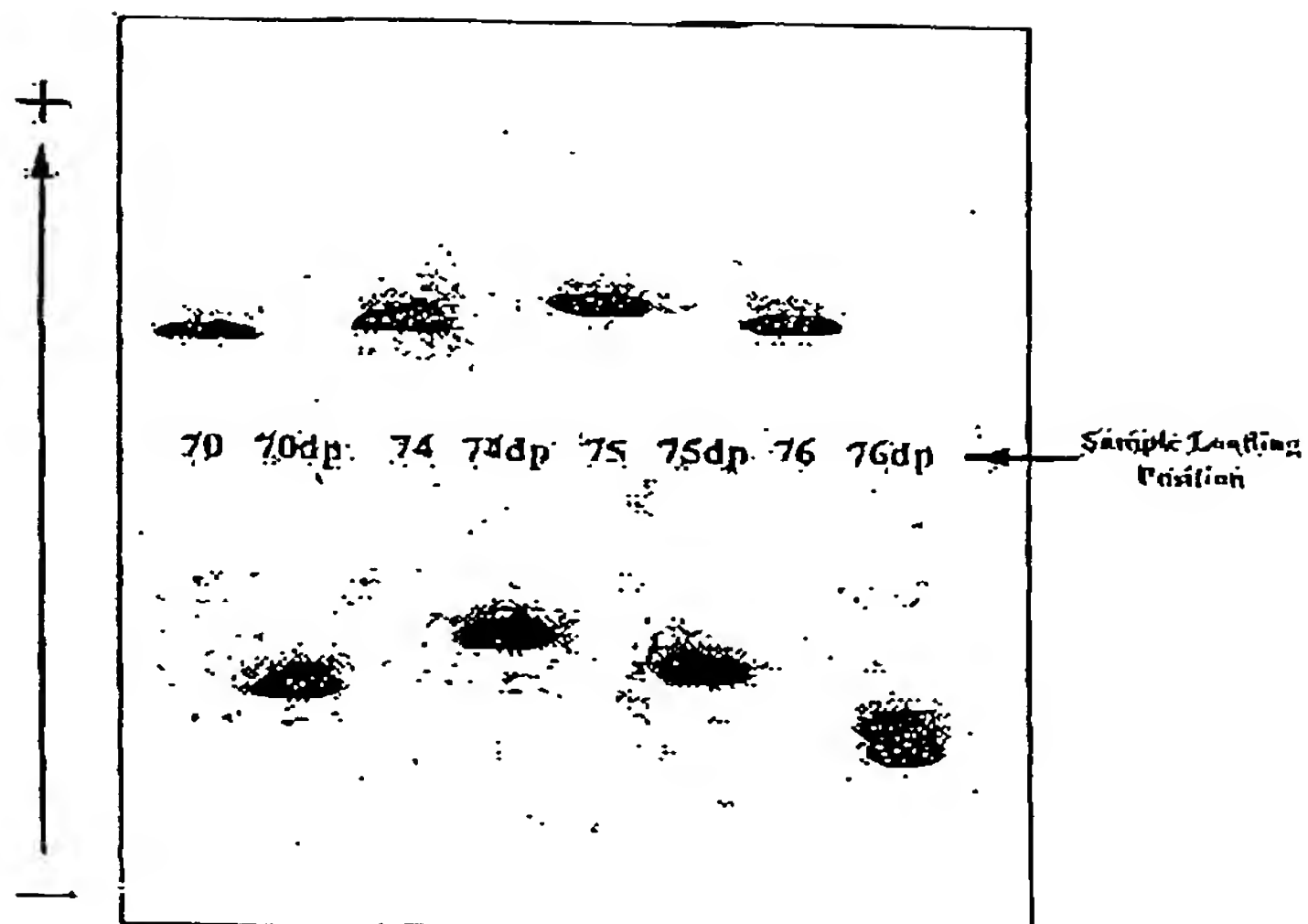


FIGURE 50

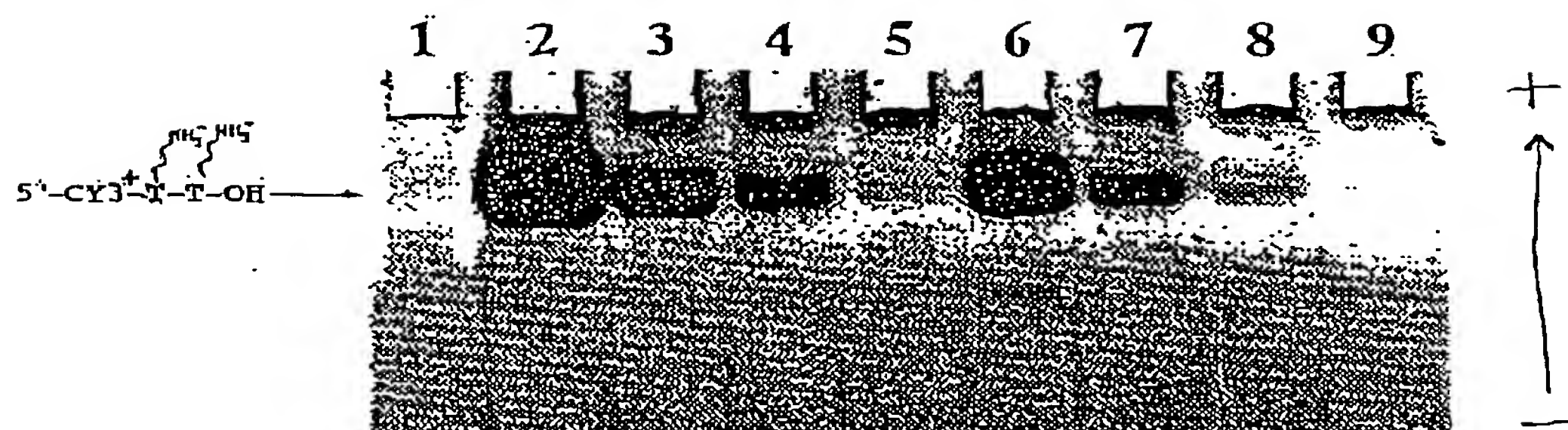


FIGURE 51

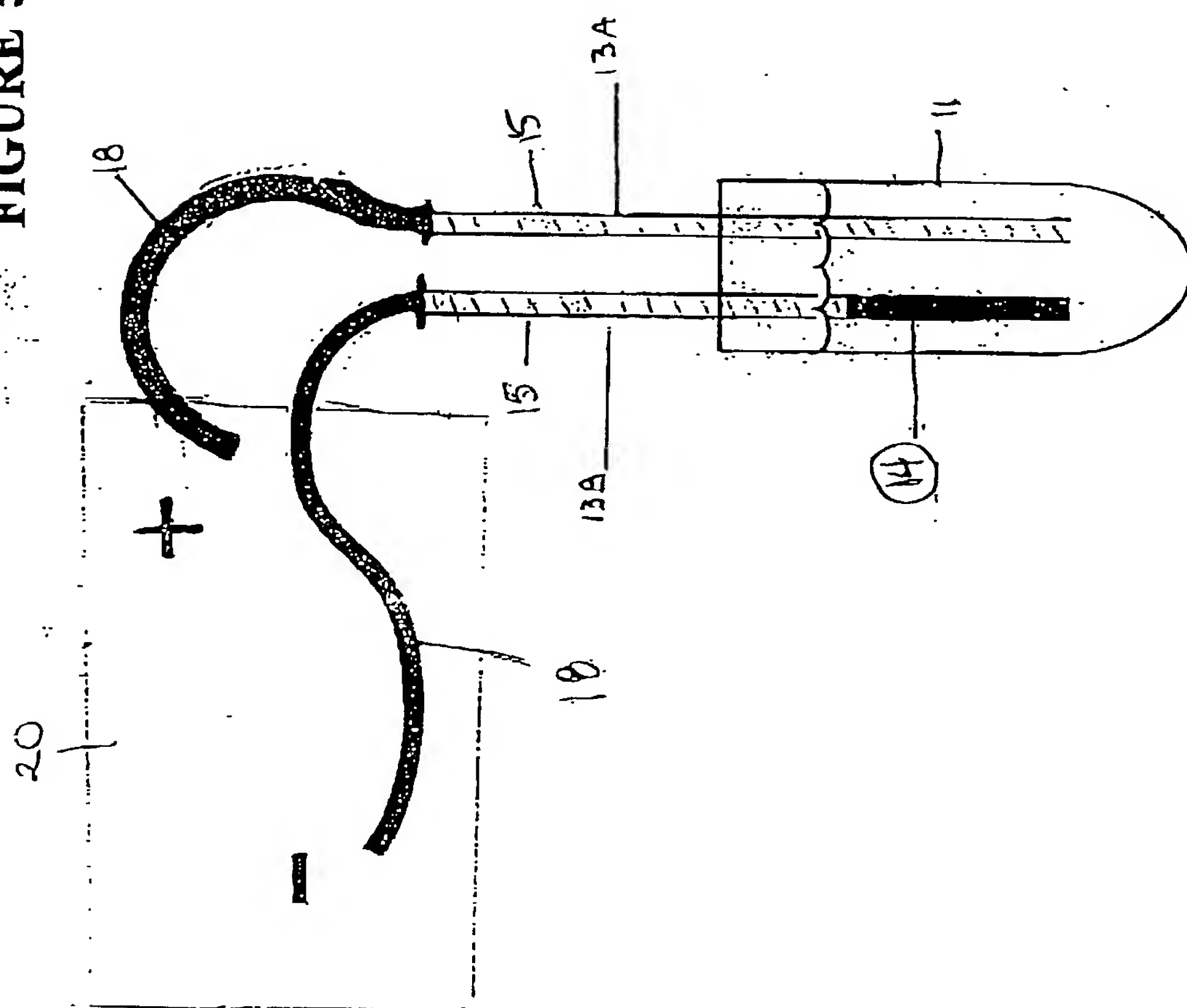
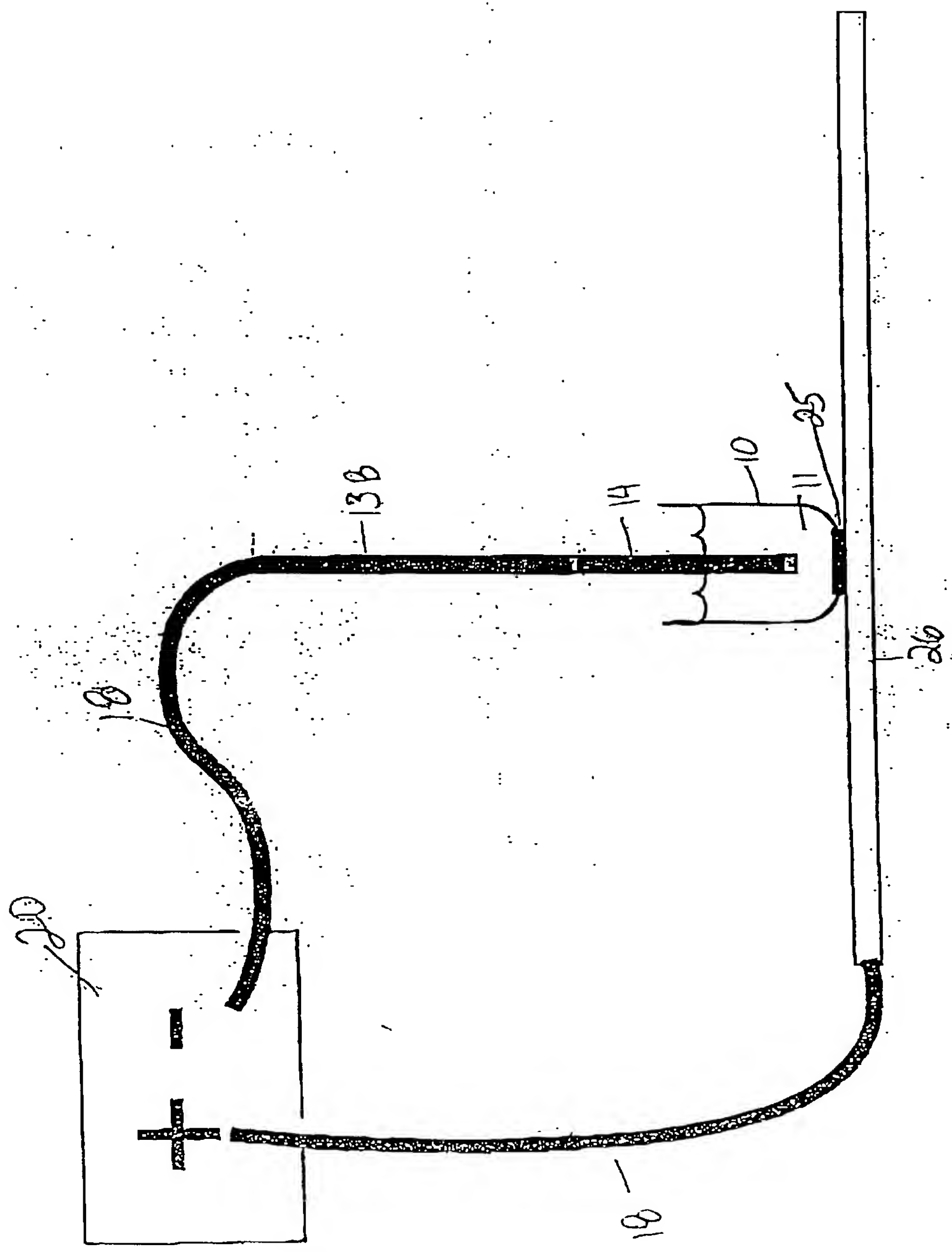


FIGURE 52





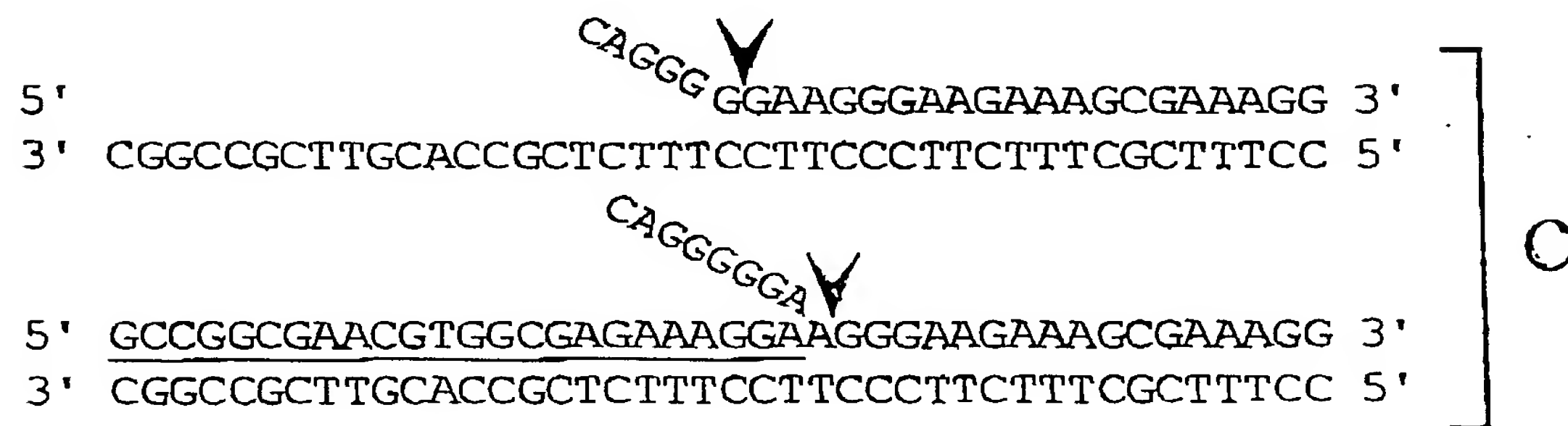
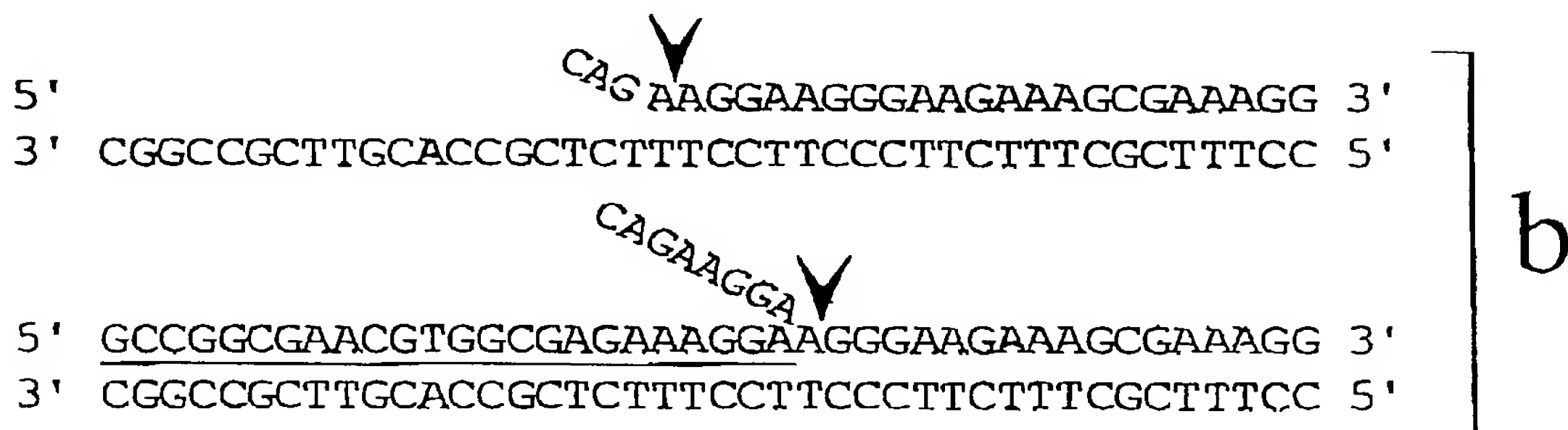
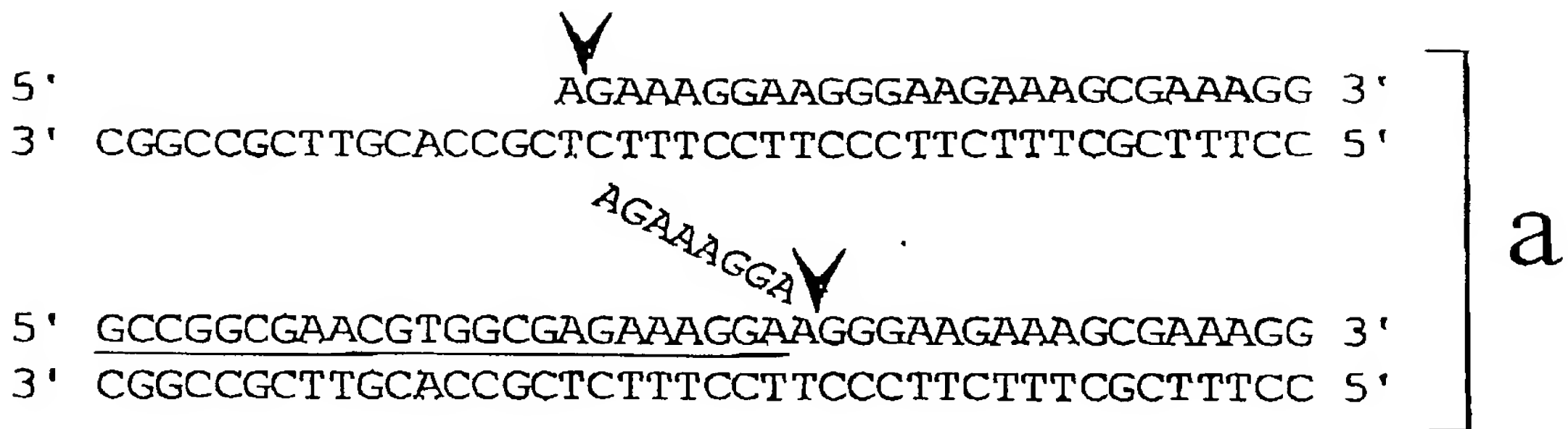
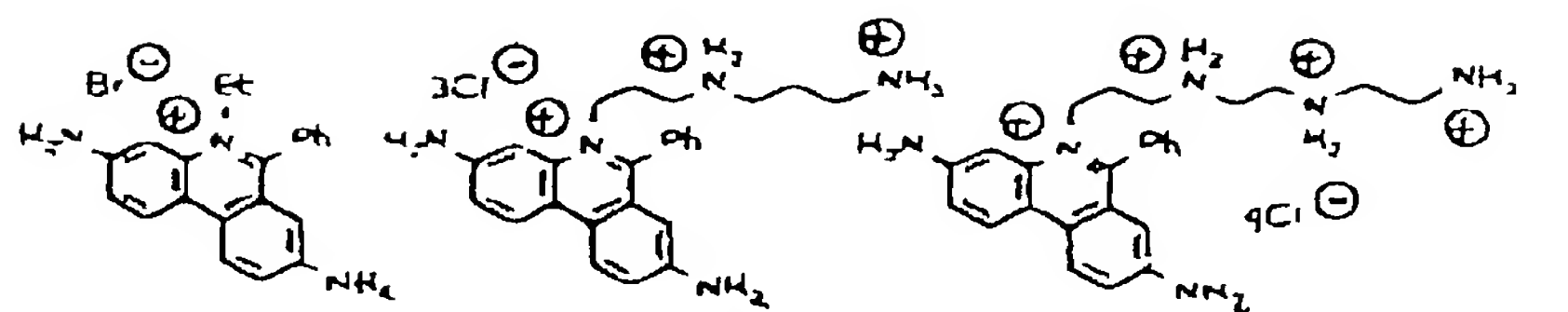
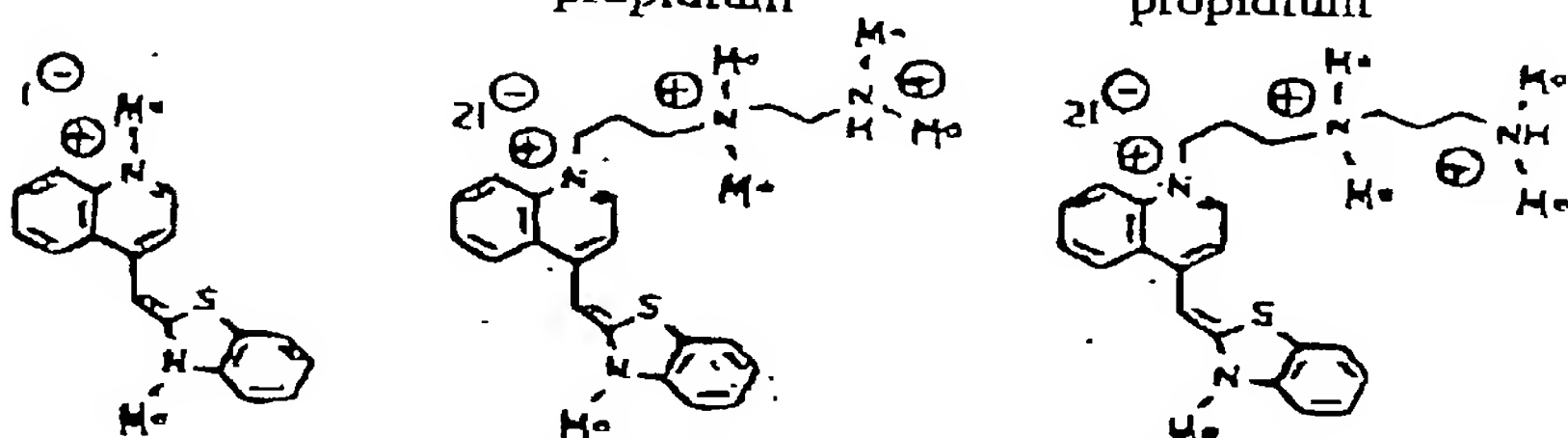


FIGURE 54

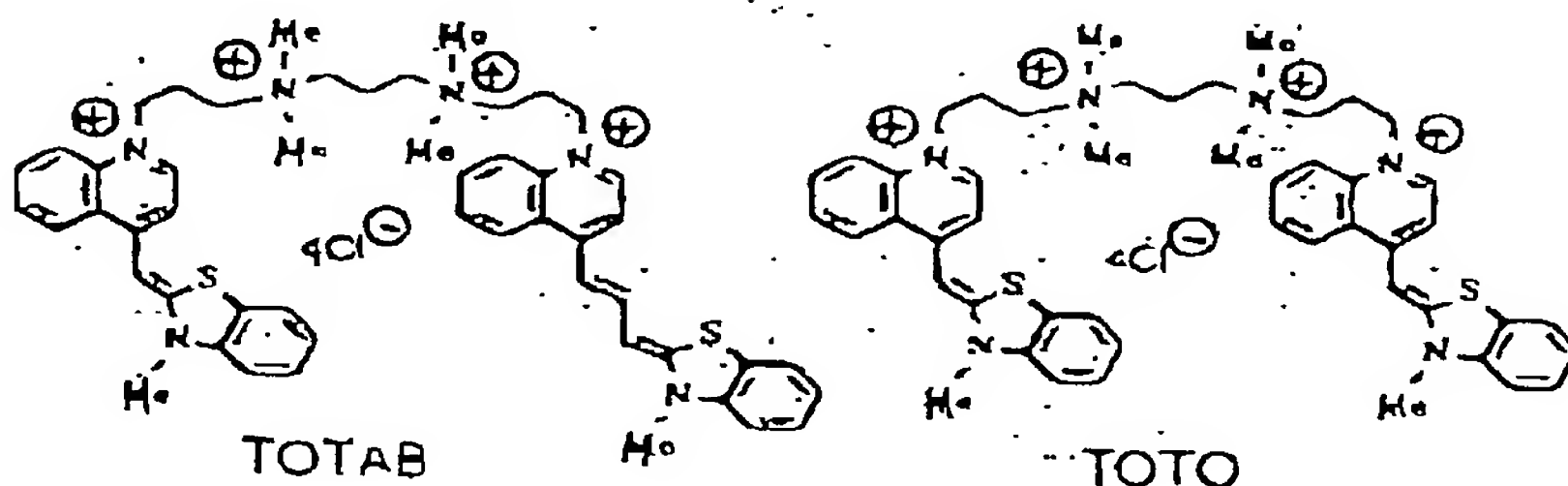
FIGURE 55



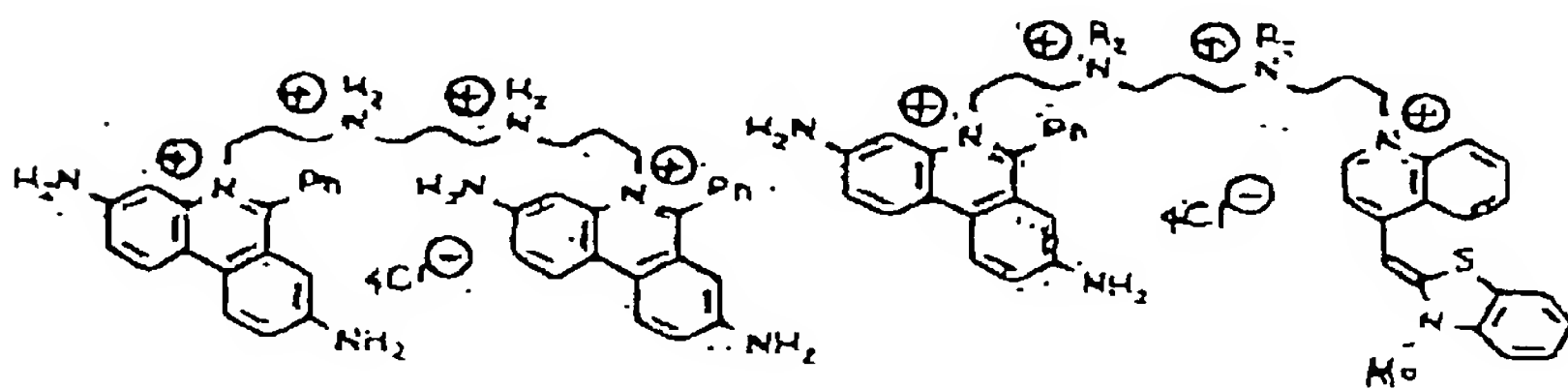
Ethidium Bromide (1,3-propanediamino)-propidium (diethylenetriamino)-propidium



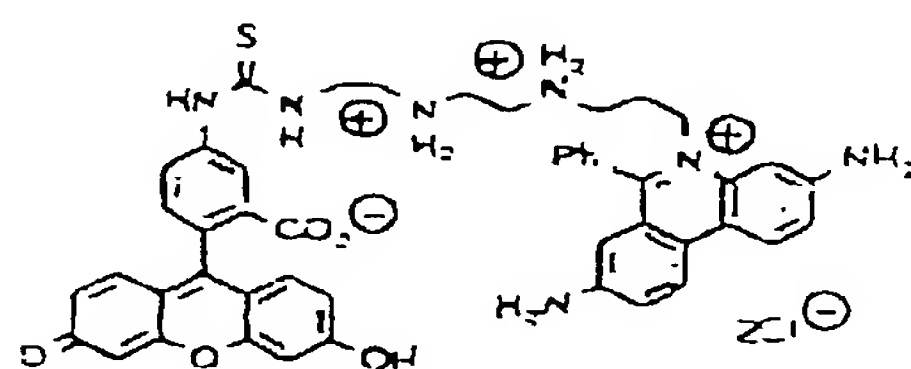
Thiazole Orange (N,N'-tetramethyl-1,2-ethanediamino)-propyl thiazole orange (N,N'-tetramethyl-1,3-propanediamino)-propyl thiazole orange



TOTAB TOTO



EtHO TOED1 (R = H) TOED2 (R = CH₃)



FED

FIGURE 5b

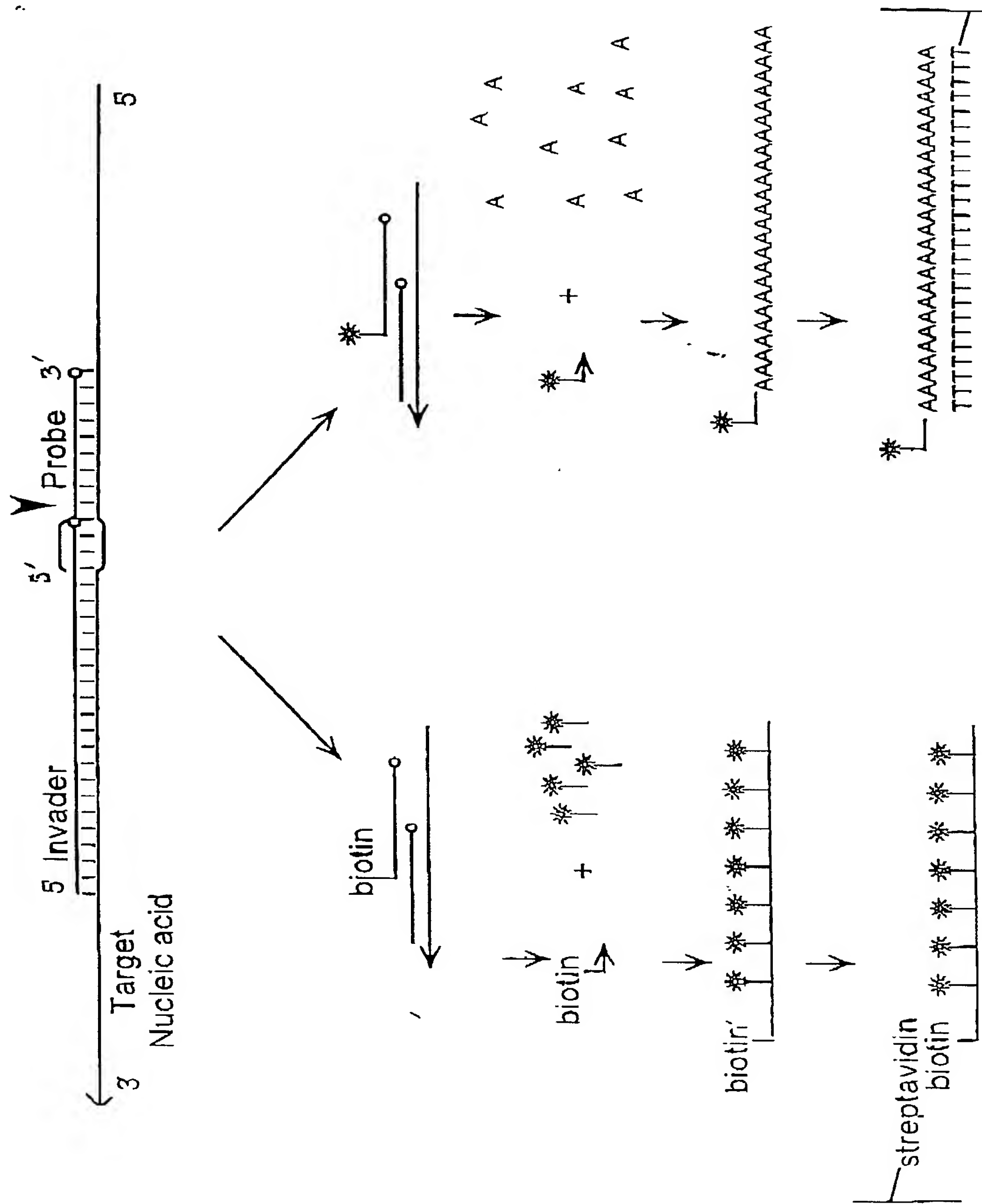


FIGURE 57

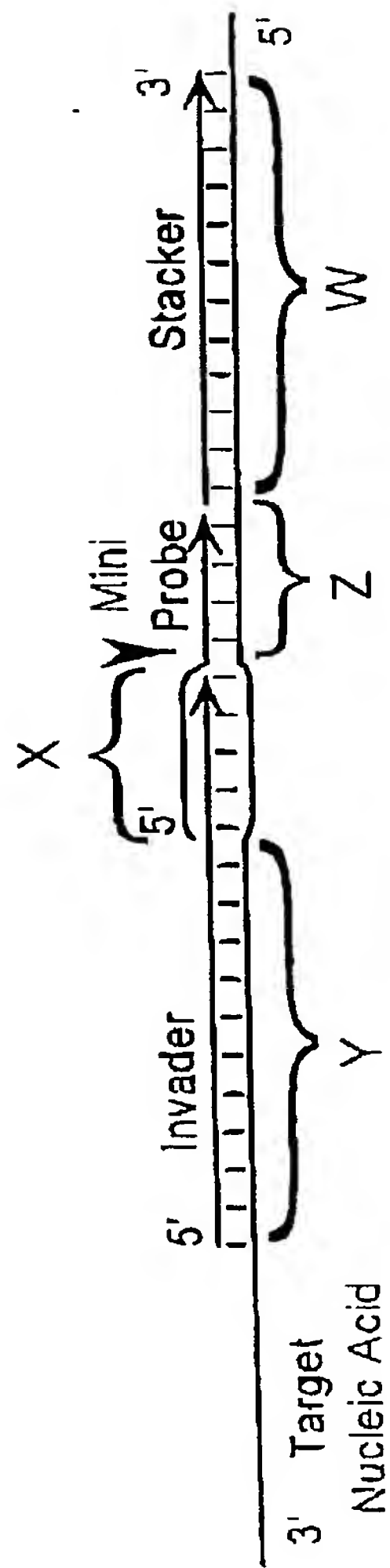


FIGURE 58



FIGURE 59A

10	20	30	40	50	60	70
-----GDFIPK	-----NIISFEDLKGGKVA	IDGMNALYQFLT	SIRLROGSPLRNRKGE	ITSA	YNGV	FY MJAFEN1.PRO
-----GEIIPR	-----KEIELENLYGKKI	AIDALNAIYQFLT	SIROKDGTP	MDSKGRIT	SHLSGLFY	PFUFEN1.PRO
-----GLAKI	ADVAPSAIRENDIKSYFGRKVA	IDASMSIYQFL	IAVRQ-GGOVL	ONEEGETT	SHLMGMFY	HUMFEN1.PRO
-----GLAK	ADVAPSAIRENDIKSYFGRKVA	IDASMSIYQFL	IAVRQ-GGOVL	ONEEGETT	S-LMGMFY	MUSFEN1.PRO
-----GLNAI	SEHVPSAIRKSOIKSFFGRKVA	IDASMSLYQFL	IAVROODGGQ	L	TNEAGETT	SHLMGMFY YST510.PRO
-----HSEFWDIAG	-----PTARPVRL	ESLEOKRMAVDAS	IWIYQFLKAVRO	DEGNVKN	-----SHITGFFR	YSTRAD2.PRO
-----SGLWNILE	-----PVKRPVKLE	TLVNRKLAIDASI	WYQFLKAVRO	KEGNOLKS	-----SHVVGFFR	SPORAD13.PRO
-----GGLWKLE	-----CSGROVS	PEALEGKILAVD	ISIWLNOALK	GVRDRHGN	STEN-----PHLLTLFH	HUMXPG.PRO
-----GGLWKLE	-----CSGHRVS	PEALEGKVLAVD	ISIWLNOALK	GVRDSHGN	VLEN-----AHLLTLFH	MUSXPG.PRO
-----GGLWKLE	-----CSGRP	INPGTLECKILAVD	ISIWLNOAVK	GARDROGNA	ION-----AHLLTLFH	XENXPG.PRO
-----GGLWKLE	-----RKVPNET	MROKTLSDIGHI	WLYESLKGCEA	HHOOT	-----PNSYLVTFFT	CELRAD2.PRO

80	90	100	110	120	130	140
-----HLLENDITPIW	VFDGEP	PKLKEKTRKVR	REMKEAE	ELKMEK	EAIKK	-----EDFEEAAKYAKRVSYLTP MJAFEN1.PRO
-----VMEAGIKPV	YVFDGEP	PEFKKKELEK	RRREAREE	AEEKWRE	ALEK	-----GEIEEARKYAORATRVNE PFUFEN1.PRO
-----RMHENG	IKPVYVFDG	CKPPOLKSGEL	AKRSERRAE	AEKLOOAA	AA	-----GAEOEVEKFTKRLVKVTK HUMFEN1.PRO
-----RMHENG	IKPVYVFDG	CKPPOLKSGEL	AKRSERRAE	AEKLOOAA	EA	-----GMEEVEKFTKRLVKVTK MUSFEN1.PRO
-----RMHENG	IKPCYVFDG	CKPPOLKSGEL	TSHELTKRSS	RRVETEK	KL	-----TTELEKMKOERRLVKVS YST510.PRO
-----RMHENG	IKPCYVFDG	CKPPOLKSGEL	TSHELTKRSS	RRVETEK	KL	-----TTELEKMKOERRLVKVS YSTRAD2.PRO
-----RMHENG	IKPCYVFDG	CKPPOLKSGEL	TSHELTKRSS	RRVETEK	KL	-----TTELEKMKOERRLVKVS SPORAD13.PRO
-----RMHENG	IKPCYVFDG	CKPPOLKSGEL	TSHELTKRSS	RRVETEK	KL	-----TTELEKMKOERRLVKVS HUMXPG.PRO
-----RMHENG	IKPCYVFDG	CKPPOLKSGEL	TSHELTKRSS	RRVETEK	KL	-----TTELEKMKOERRLVKVS MUSXPG.PRO
-----RMHENG	IKPCYVFDG	CKPPOLKSGEL	TSHELTKRSS	RRVETEK	KL	-----TTELEKMKOERRLVKVS XENXPG.PRO
-----RMHENG	IKPCYVFDG	CKPPOLKSGEL	TSHELTKRSS	RRVETEK	KL	-----TTELEKMKOERRLVKVS CELRAD2.PRO

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FIGURE 59B

150 160 170 180 190 200 210
130 WVENCK'LLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLITTKEM---- MJAFEN1.PRO
131 LIEDAK'LLLELMGIPIVOAPSEGEAQAAAYMAAKGSVYASASQDYDSLLFGAPRLVRNLITIGKRKLPGK PFUFEN1.PRO
132 HNDECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ HUMFEN1.PRO
133 HNDECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ MUSFEN1.PRO
134 HVEEAOKLLGLMGIPYIAPTAEAOCAELAKKGKVYAAASEMDILCYRTPFLRLRHLTFSEAKKEPIH YST510.PRO
135 HKEVOELLSRFGIPYITAPMEAEAOCAELQLNLVDGII TDDSDVFLFGGTKIYKNMFHEKNY---VE YSTRAD2.PRO
136 HKECOELLRLFGIPYIVAPOEAEAOCSKLELKLVDGIVTDDSDVFLFGGTRVYRNMFNQNKF---VE SPORAD13.PRO
137 HFELESCELLRLFGIPYIOAPMEAEAOCAILDLTDOTSGTITDDSDIWLFGARHVYRNFFNKNKF---VE HUMXPG.PRO
138 HFELESCELLRLFGVPIIOAPMEAEAOCAVLDLSDOTSGTITDDSDIWLFGARHVYKNFFNKNKF---VE MUSXPG.PRO
139 HFELESCELLRLFGIPYIVAPMEAEAOCAILDLTDOTSGTITDDSDIWLFGARHVYKNFFSONKH---VE XENXPG.PRO
140 HFKY'NALLTELGIKVIAPGDGEAOCARIEOLGVTSGCITTDYDFLFGGKNLYRFDFTAGT----- CELRAD2.PRO

220 230 240 250 260 270 280
141 -----PELIELNEVLEDLRLSLDQLIDIAIFMGTOYNPGGV--K--GIGFKRAYELVRSGVAK--DV MJAFEN1.PRO
142 HVE-IPPEL:ILEEVVKELKLTREKLIELAILVGTOYNPGGI--K--GIGLKKALEIVRHSKOPLAKF PFUFEN1.PRO
143 HSLSRILOEGLNOEOFVOLCILLGSDYCESIRGIGPKRAVOLIOK--HKSIEEIVRRLDPN-----KY HUMFEN1.PRO
144 HSLSRVLCEGLNOEOFVOLCILLGSDYCESIRGIGAKRAVOLIOK--HKSIEEIVRRLDPS-----KY MUSFEN1.PRO
145 HSELVLRGLDLTIEQFVOLC:MLGCDYCESIRGVGPVTALKIKT--HGSIEKIVEFIESGESNNTKW YST510.PRO
146 HCAESILKLLGLDRKNMIELAQLLGSDYINGLKMGMPVSSIEVIAEF---GNLKNFKDWYNNNGOFDKRK YSTRAD2.PRO
147 HMDOMKREFNVNOMDLJKLAHLLGSDYTMGLSRVGPVLALEILHEFPDGLTFEKKWFORLSTGHAS SPORAD13.PRO
148 HGYDFHNOGLDRNKLINLAYLLGSDYTEGIPYVGCVTAMEILNEFPBGHGLEPLLKFESEWHEAOKNP HUMXPG.PRO
149 HGYDFYSOLGLDRNKLINLAYLLGSDYTEGIPYVGCVTAMEILNEFPGRGLDPLLKFESEWHEAONNK MUSXPG.PRO
150 HGYDFHNOGLDRSKLINLAYLLGSDYTGIPYVGVVSAMEILNEFPGGGLEPLVKFEWSEWSEAOOKD XENXPG.PRO
151 -----SSTACLHDIHLSLGRMF----- CELRAD2.PRO

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FIGURE 59C

	290	300	310	320	330	340	350
1	REVEVYDETKR1FKEPKV	----	----	----	TD--	NYSLSKLPDKEGI	KFLVDENDFNVD MJAFEN1.PRO
2	SDVDLYAIKEFFLNPPV	----	----	----	TO--	NYNLVWRPDEEGIL	KFLCDEHDFSEE PFUFEN1.PRO
3	PENWLHKEAHOLFLEPEV	----	----	----	LOPES	VELKWSEPNEEEL	IKFMCGEKOFSEE HUMFEN1.PRO
4	PENWLHKEAOLLEPEV	----	----	----	VOPE	VELKWSEPNEEEL	VKFMCGEKOFSEE MUSFEN1.PRO
5	PEDWPKYKCARMLFLOPEV	----	----	----	JDGNE	INLKWSPPKKEKE	IEYLCDDKKFSEE YST510.PRO
6	ETENKFEKDLRKKLVNNEI	ILDDF	PSVMVYOAYMRPE	VDHOTT	PFVWGV	POLOMLRSFMK	TOLGWPHE YSTRAD2.PRO
7	QVNTPVKKRINKLVGK-I	ILPSE	FPNPLVDEAYLHP	AVDDSK	SFOWGIP	DLROFLMATV	GWSKO SPORAD13.PRO
8	RPNPHDTKVKKK--	RTLQ	LTGFPNPAVAEAYL	KPVVDD	SGSFLWGK	PDLOKIREFC	ORYFGWNRT HUMXPG.PRO
9	RENPYDTKVKKK--	RKLQ	LTGFPNPAVADAYL	RPVVDD	SRGSFLWGK	PDVDKIREFC	ORYFGWNRM MUSXPG.PRO
10	RPAPNDTKVKKK--	RLDQ	OSFPNPAVASAYL	KPVVDE	SKSAF	SWGRPDLEQIRE	FCESRFGWYRL XENXPG.PRO
11	----	EKKV	SRPHLISTAIL	LGCDYFORGV	ONIGIVSVFO-IL	GEFGDDGNEE	IOPHVILDRFASYVRE CELRAD2.PRO

	360	370	380	390	400	410	420
1	PKKHVDKLYNLIA	----	----	----	----	----	----
2	ANGLERLKKAI	----	----	----	----	----	----
3	PSGVKRLSKSROGS	-TOGR	LDFFKVT	----	----	----	----
4	PSGVKRLSKSROGS	-IQGR	LDFFKVT	----	----	----	----
5	PSGISRLKKGLKSG	-IQGR	LDGFFOVV	----	----	----	----
6	DELLIPLIRDVNKRKK	----	----	----	----	----	KGKO YSTRAD2.PRO
7	DELLIPLIRDVNKRKK	----	----	----	----	----	VGTO SPORAD13.PRO
8	DESLFPYLKOLDAOOT	LRID	SFFRLA	OOEKEDAKRI	KSORL	NRAVTCMLR	KEKEAASEIEAVSVAM HUMXPG.PRO
9	DESLYPYLKHLNAHOT	LRID	SFFRLA	OOEKODAKL	IKSHR	LSRAVTCMLR	KEREKAPELTKVTEAM MUSXPG.PRO
10	DESLFPYLKOLNAOOT	LRID	SFFRLA	OOEHEAAG--	LKSOR	LRRAVTCMKR	KERDOVEAEVEAAVAM XENXPG.PRO
11	DESEETAPKLRRLR	KKYNF	PVGF	PNCOAVHNAIT	MYLR	PPVSSEIPKIPR	----AANFOOVAEIM CELRAD2.PRO

FIGURE 59D

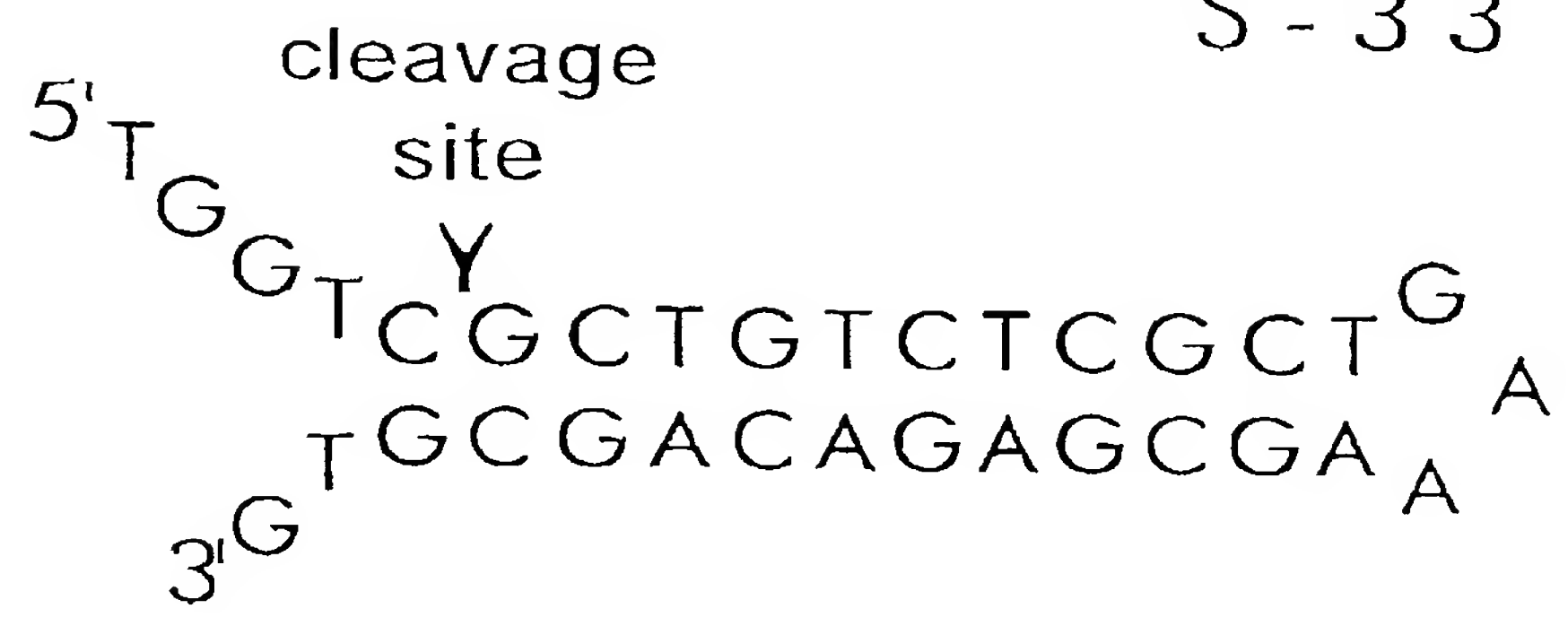
	430	440	450	460	470	480	490
1	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
2	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
3	-----	-----	-----	-----	-----	-----	HUMFEN1.PRO
4	-----	-----	-----	-----	-----	-----	MUSFEN1.PRO
5	-----	-----	-----	-----	-----	-----	YST510.PRO
6	-----	-----	-----	-----	-----	-----	YSTRAD2.PRO
7	-----	-----	-----	-----	-----	-----	SPORAD13.PRO
8	-----	-----	-----	-----	-----	-----	HUMXPG.PRO
9	-----	-----	-----	-----	-----	-----	MUSXPG.PRO
10	-----	-----	-----	-----	-----	-----	XENXPG.PRO
11	-----	-----	-----	-----	-----	-----	CELRAD2.PRO

	500	510	520	530	540	550	560
1	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
2	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
3	-----	-----	-----	-----	-----	-----	HUMFEN1.PRO
4	-----	-----	-----	-----	-----	-----	MUSFEN1.PRO
5	-----	-----	-----	-----	-----	-----	YST510.PRO
6	-----	-----	-----	-----	-----	-----	YSTRAD2.PRO
7	-----	-----	-----	-----	-----	-----	SPORAD13.PRO
8	-----	-----	-----	-----	-----	-----	HUMXPG.PRO
9	-----	-----	-----	-----	-----	-----	MUSXPG.PRO
10	-----	-----	-----	-----	-----	-----	XENXPG.PRO
11	-----	-----	-----	-----	-----	-----	CELRAD2.PRO

7c

FIGURE 60

S - 3 3



1 1 - 8 - 0

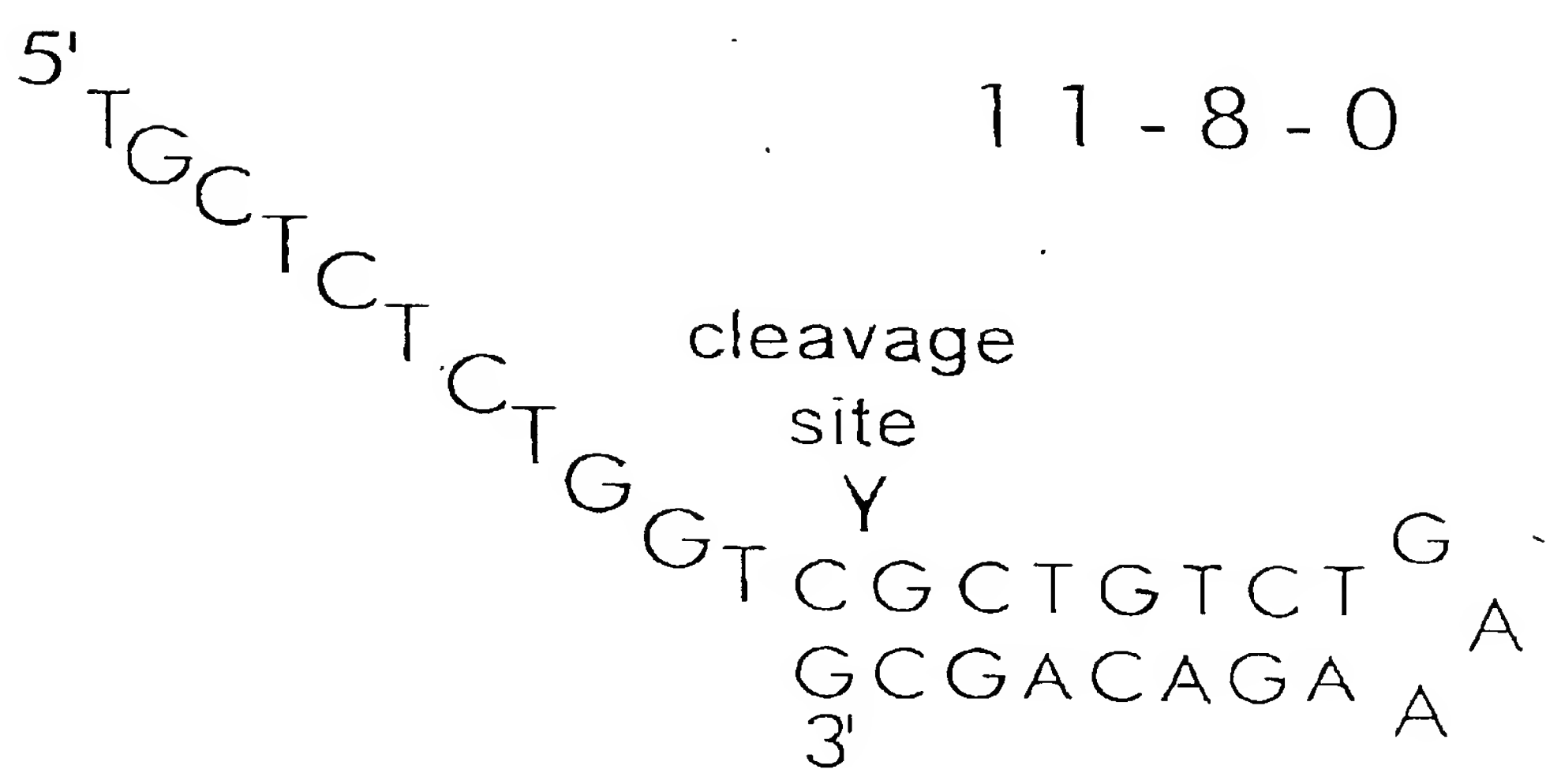
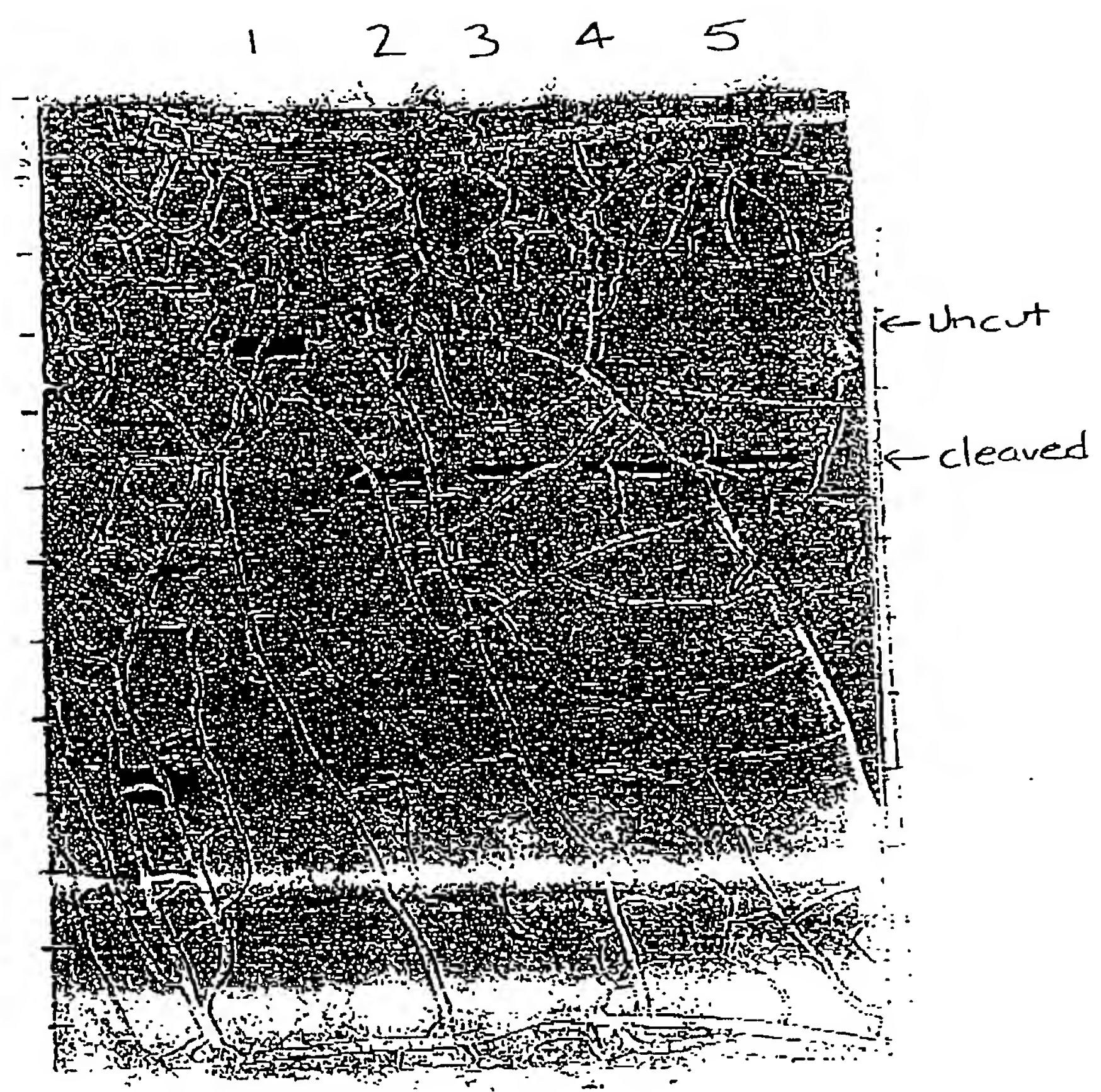
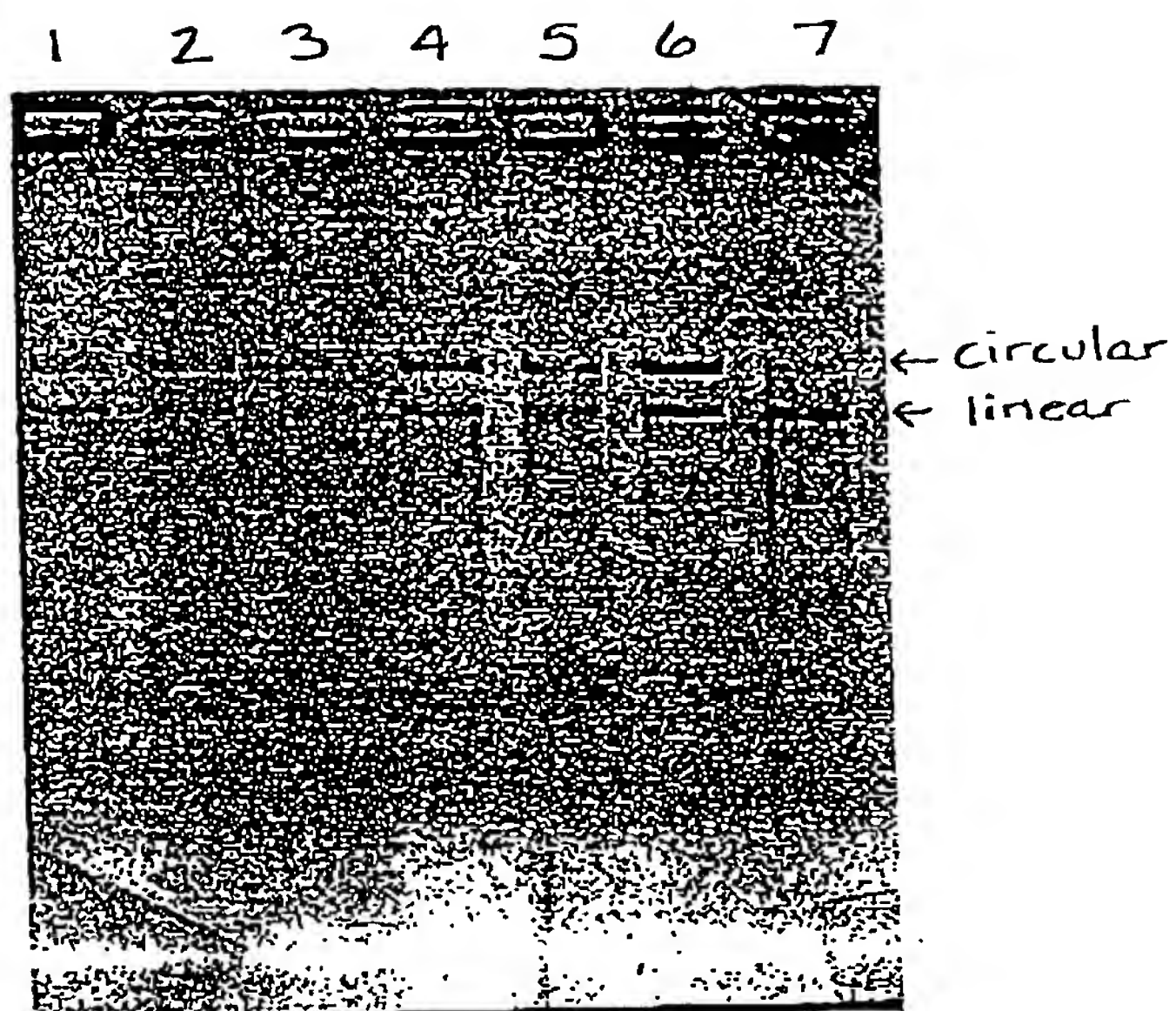


FIGURE 61



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FIGURE 63



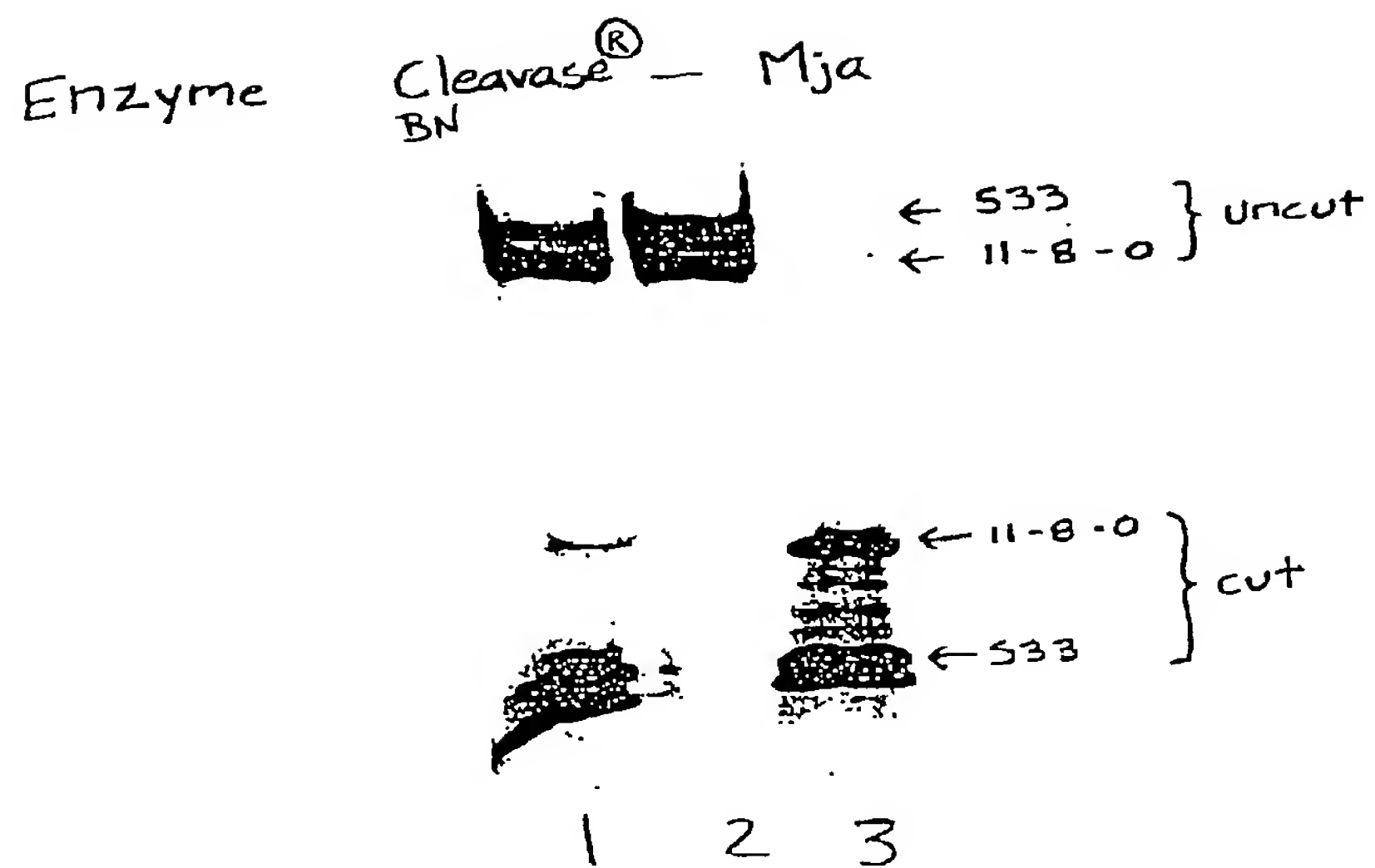


FIGURE 65

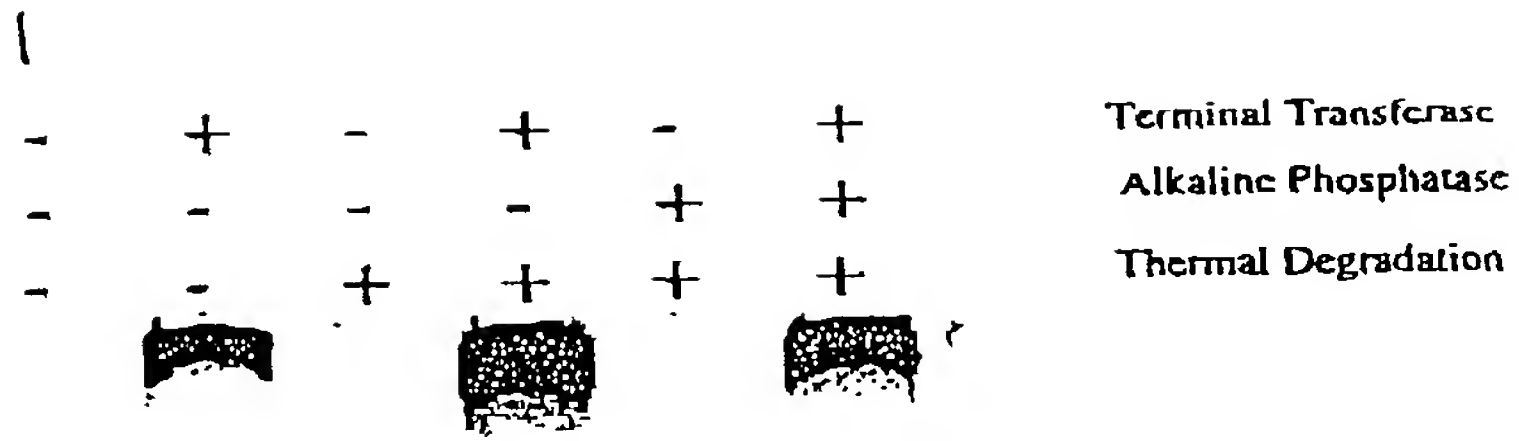


FIGURE 66

5'-nAGAAAggaaggga agaaagcgaaagG-3'

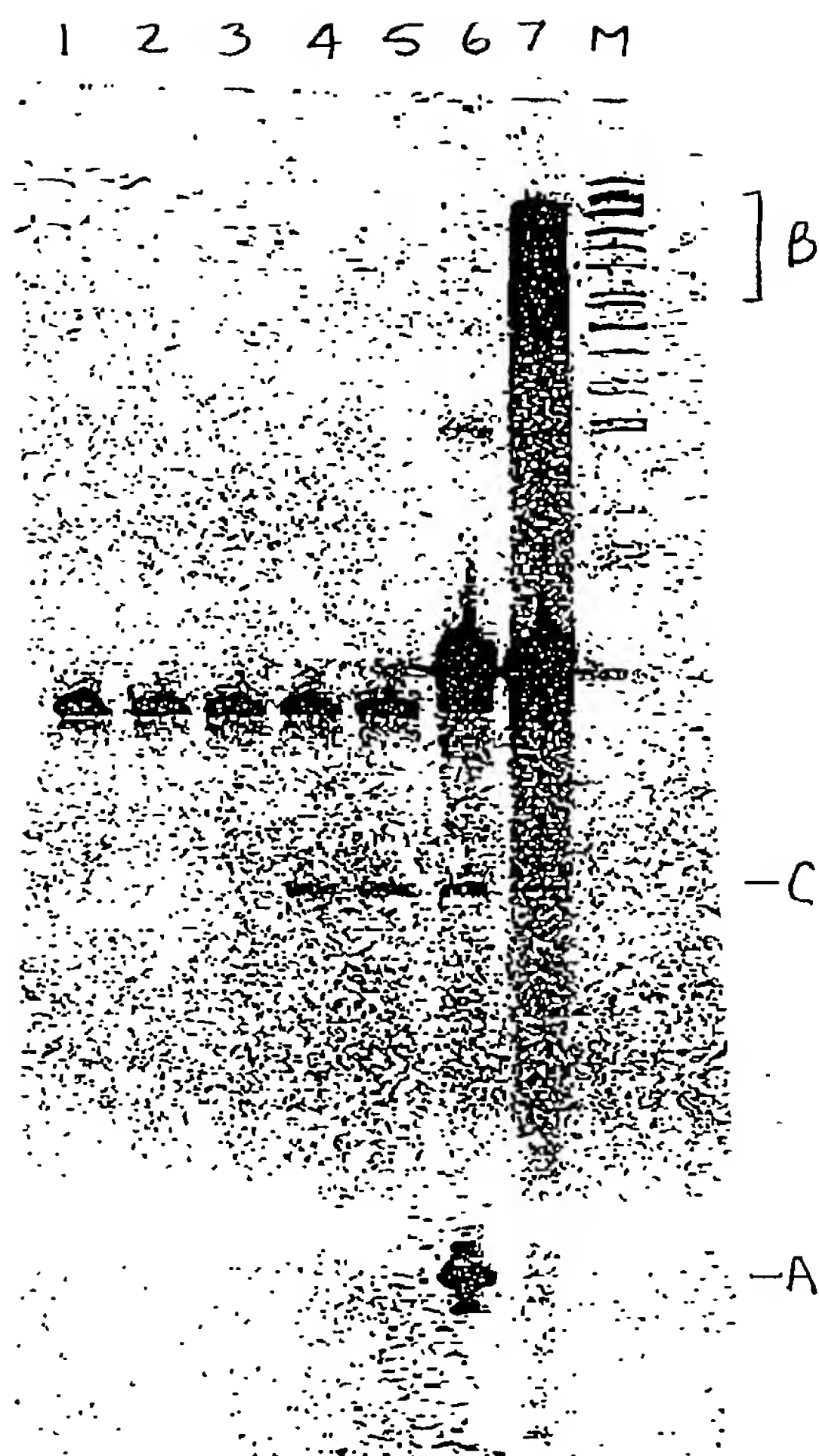
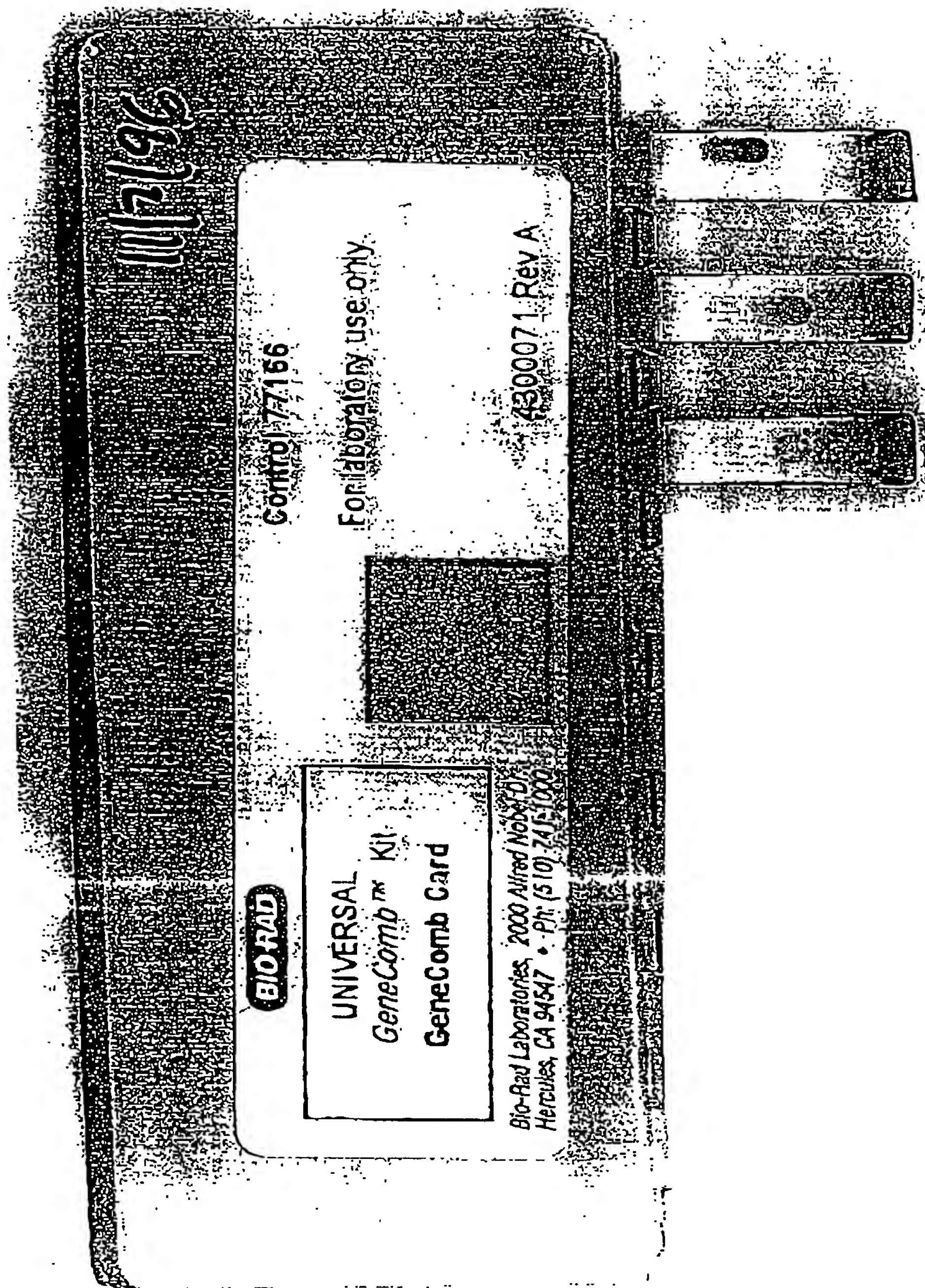


FIGURE 67

FIGURE 68

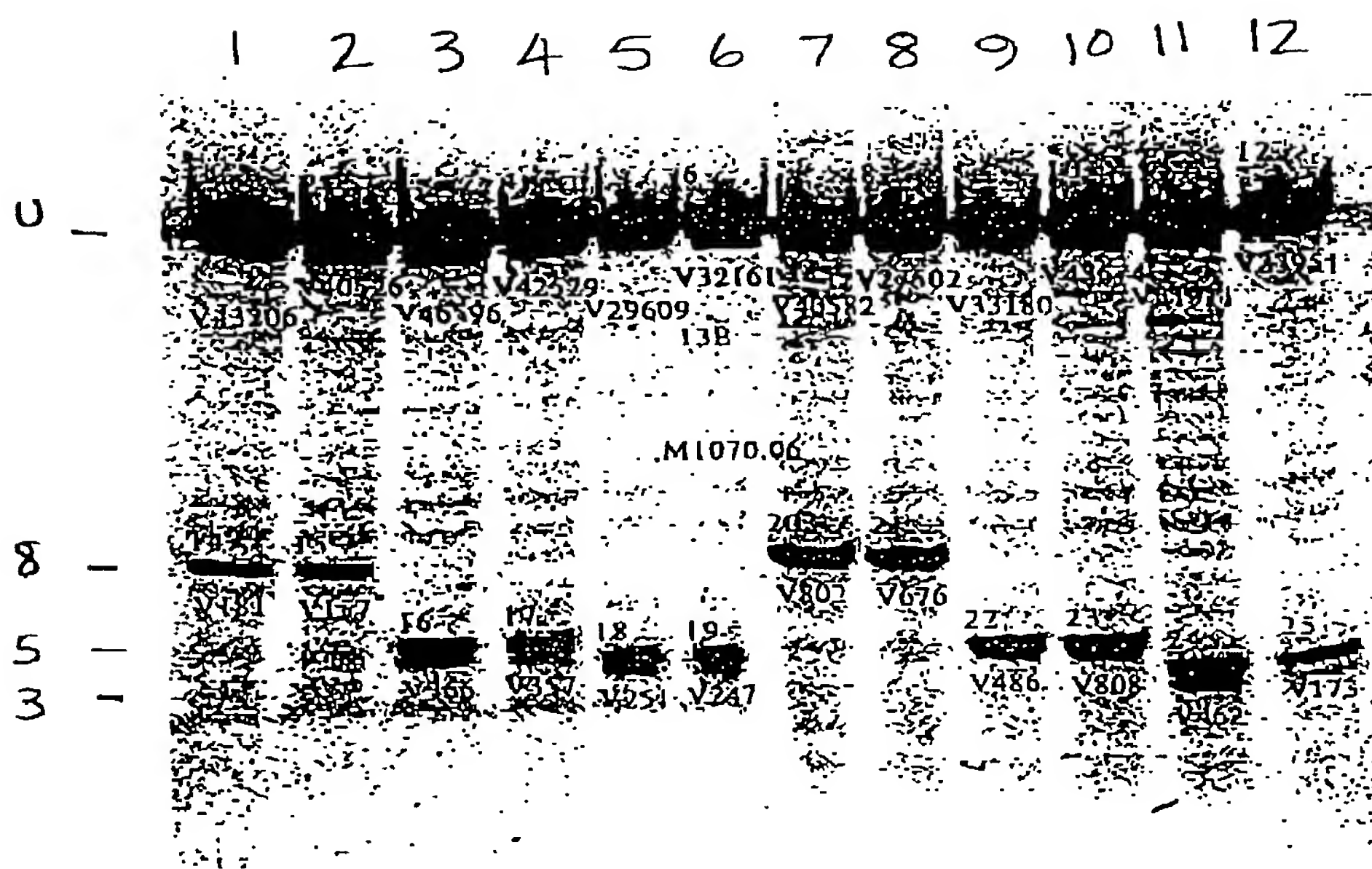


8

7

6

FIGURE 69



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FIGURE 70

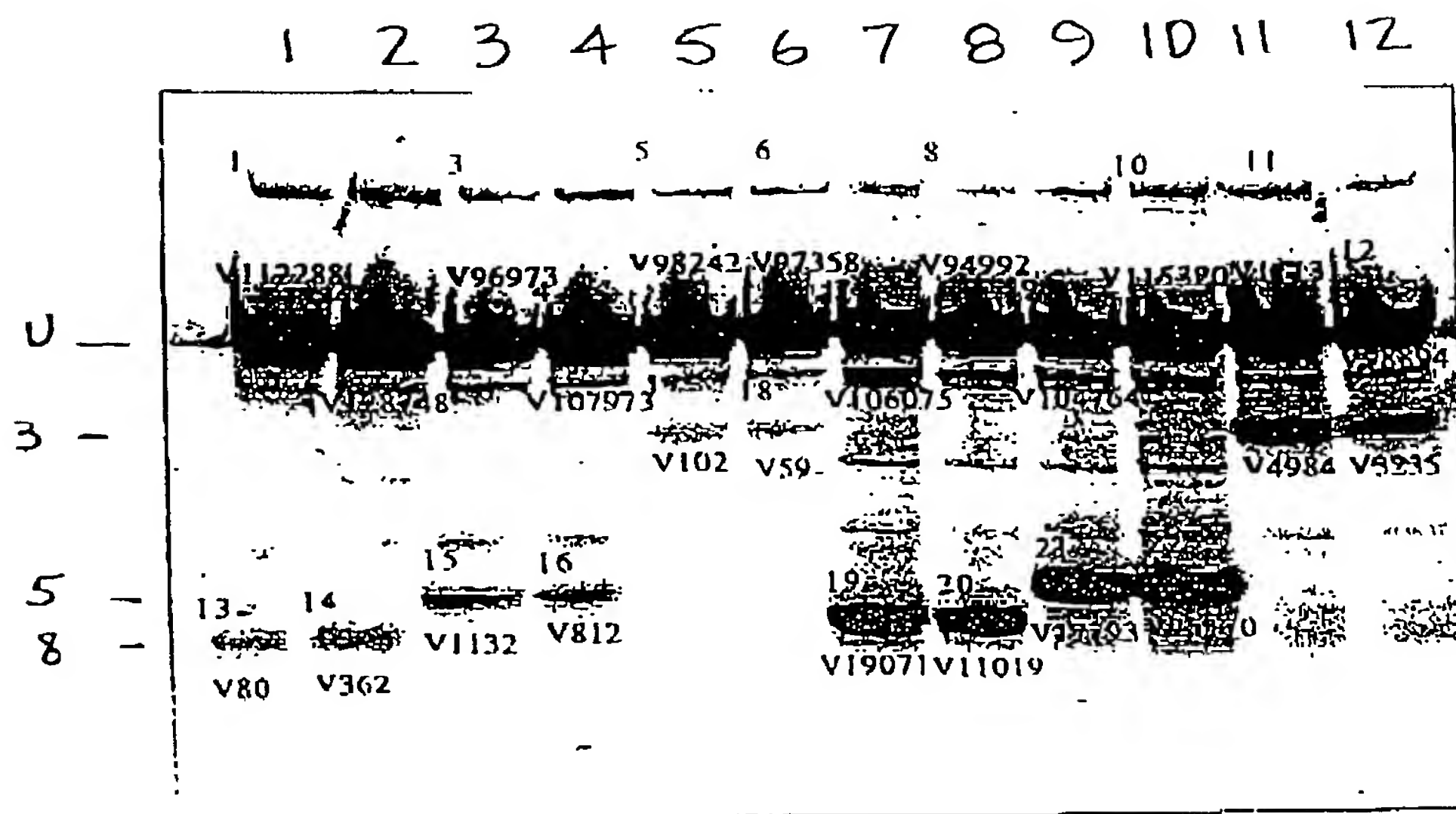
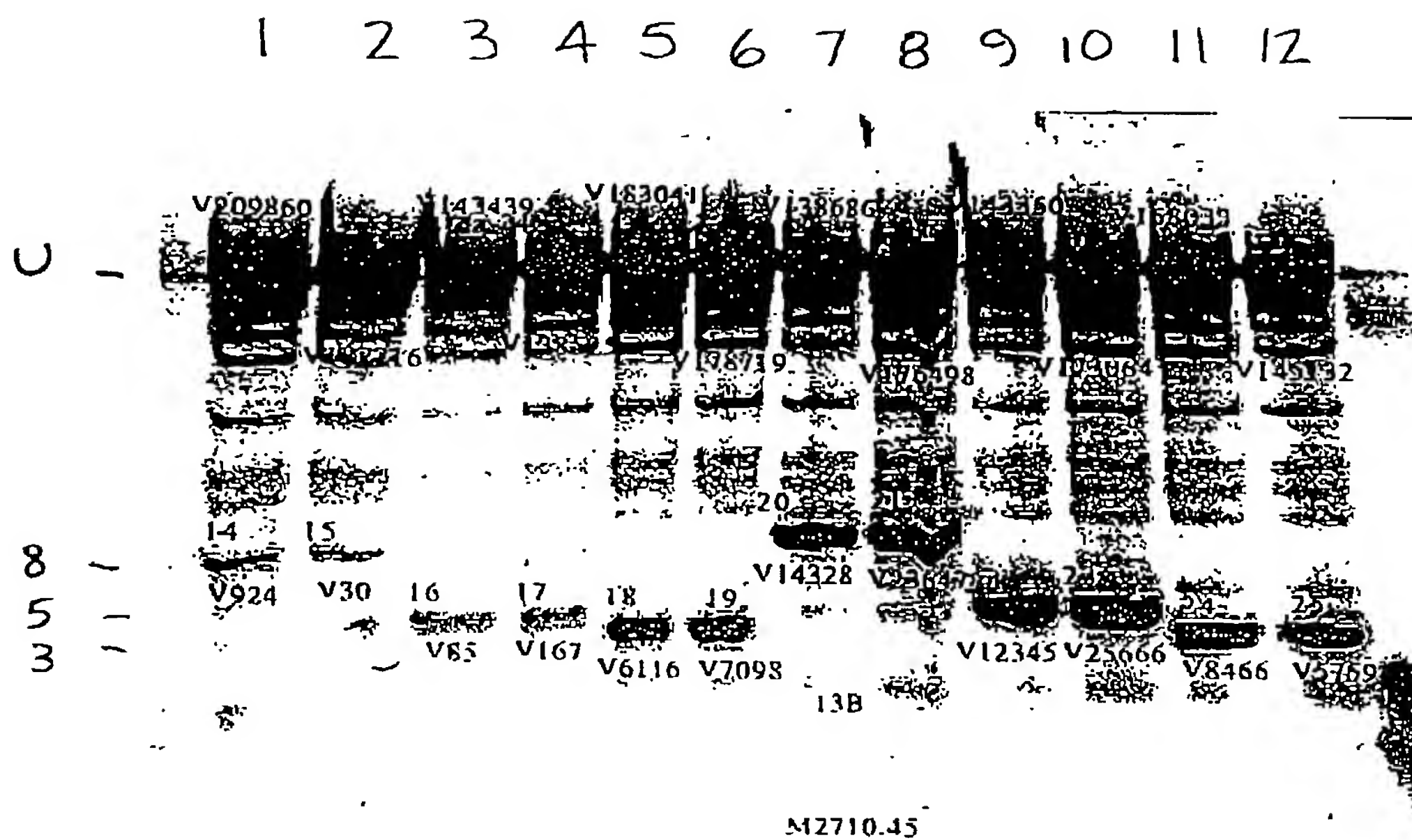
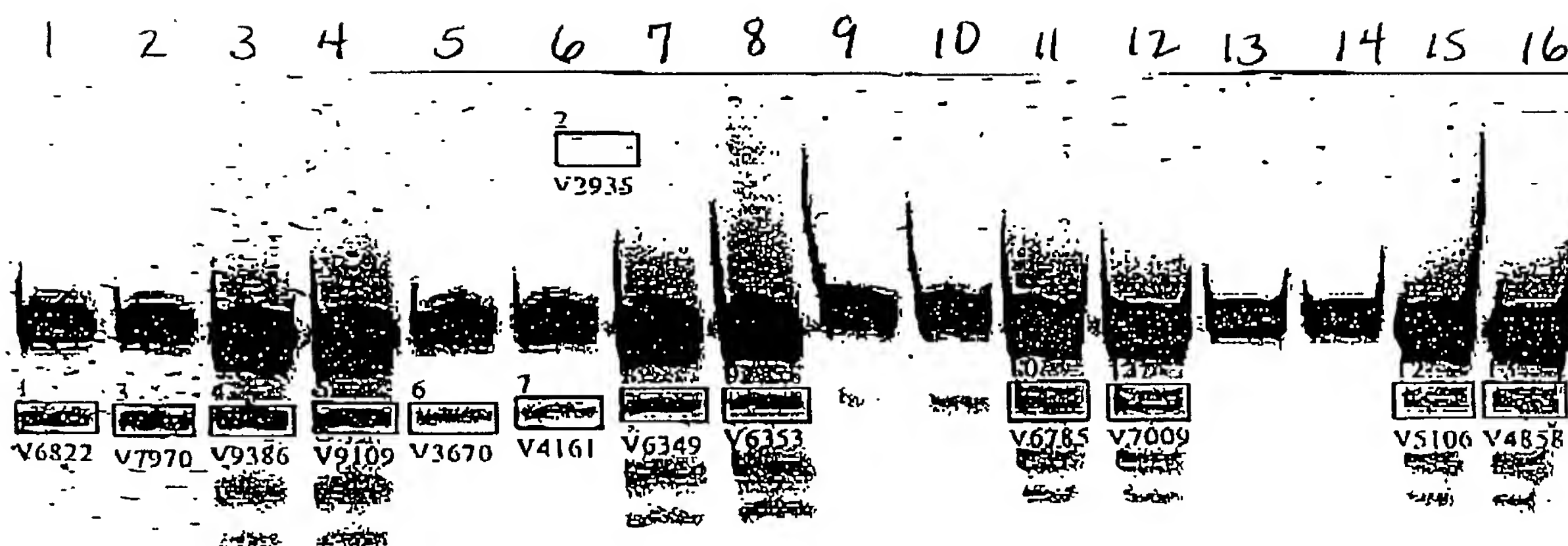


FIGURE 71



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A



B

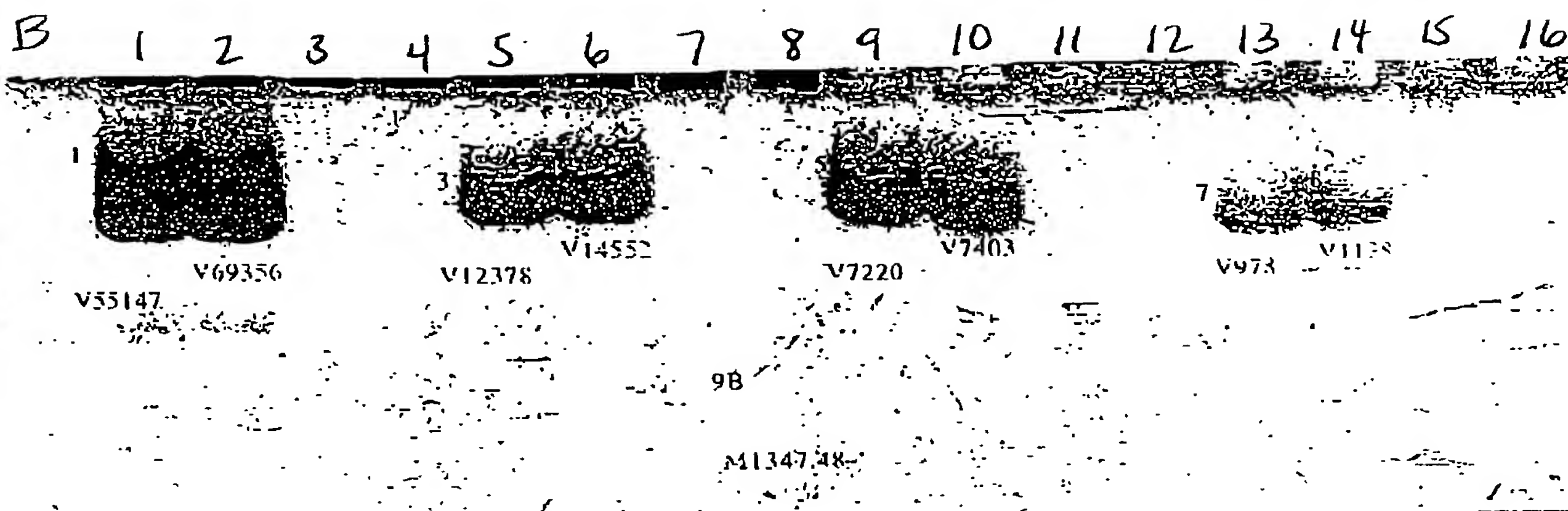
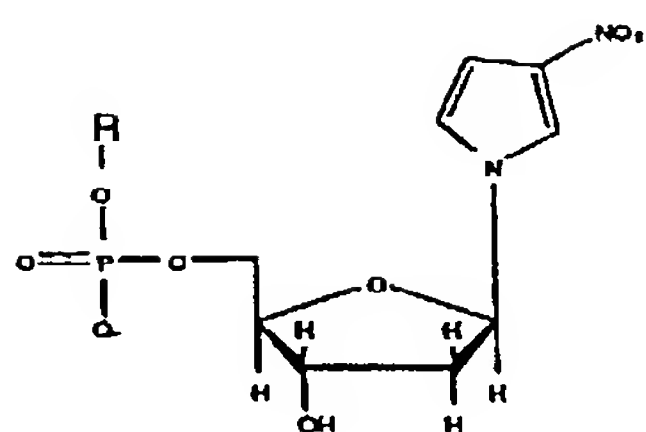


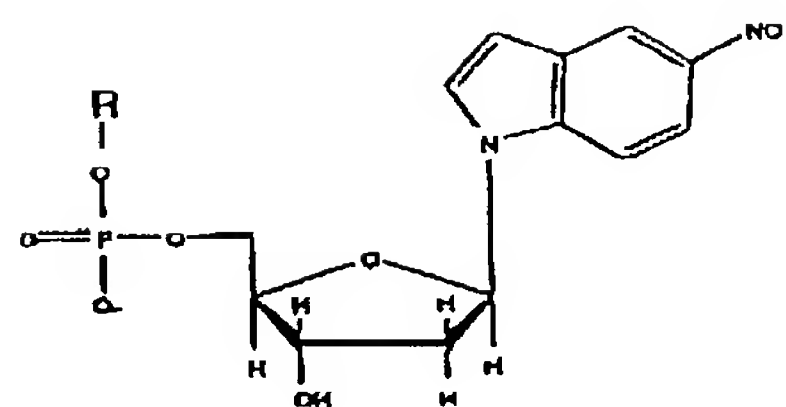
FIGURE 72

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FIGURE 73



3-nitropyrrole



5-nitroindole

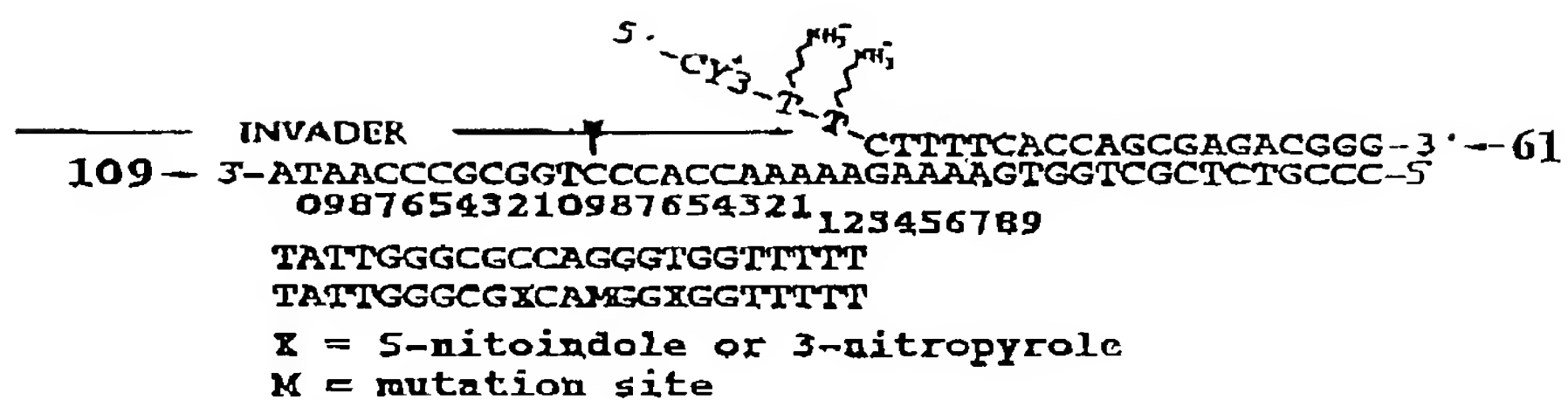


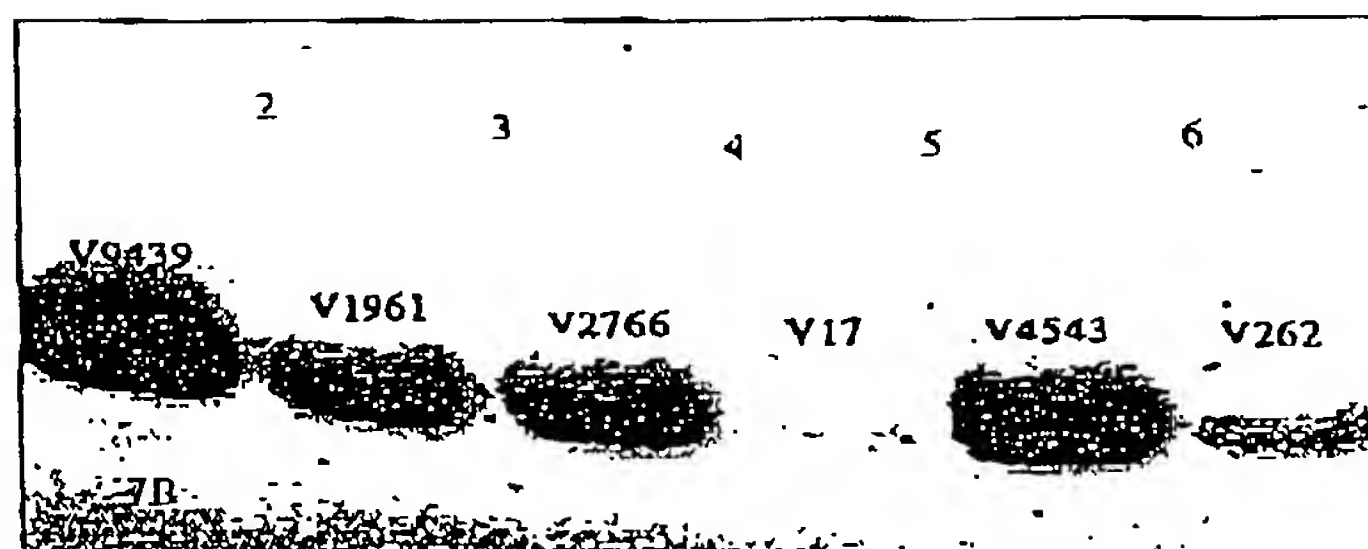
FIGURE 74

All Comp	1 Base Mismatch	All Comp	1 Base Mismatch	All Comp	1 Base Mismatch
		2 NI	2 NI	1 NP	1 NP

Inval #	67	114	115	116	112	113
------------	----	-----	-----	-----	-----	-----

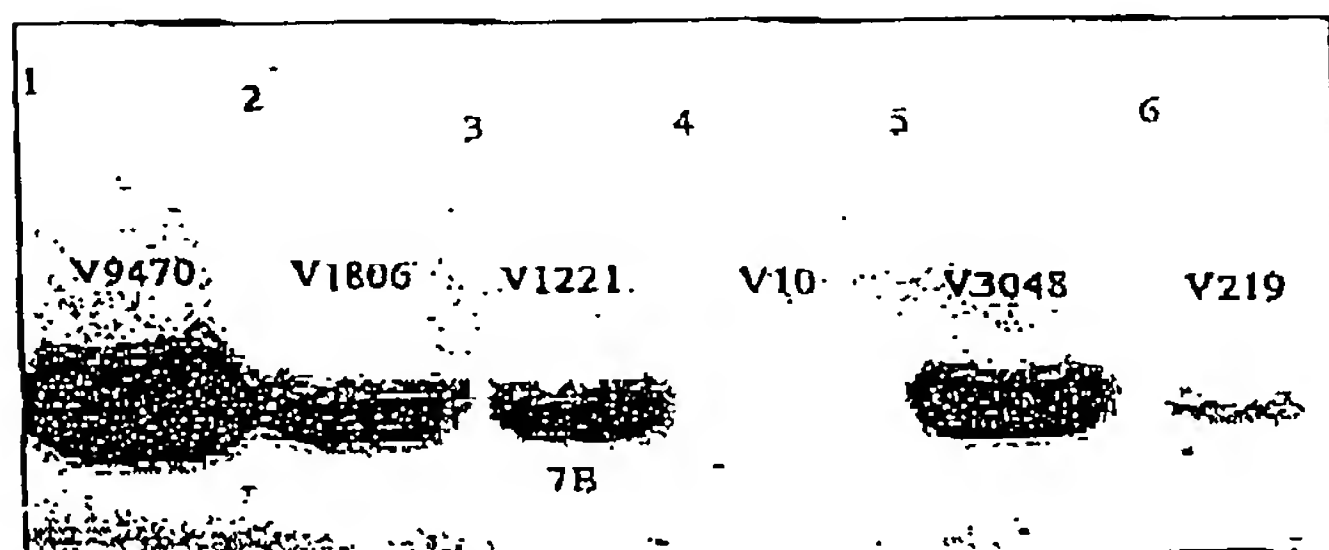
A

52°C



B

55°C



C

58°C

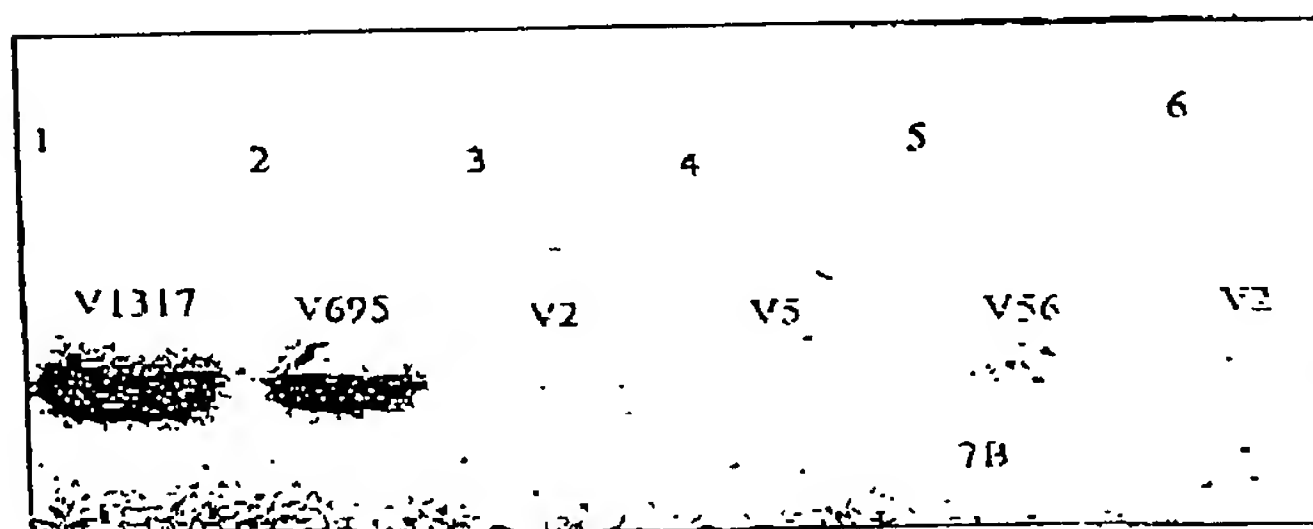


FIGURE 75

FIGURE 76

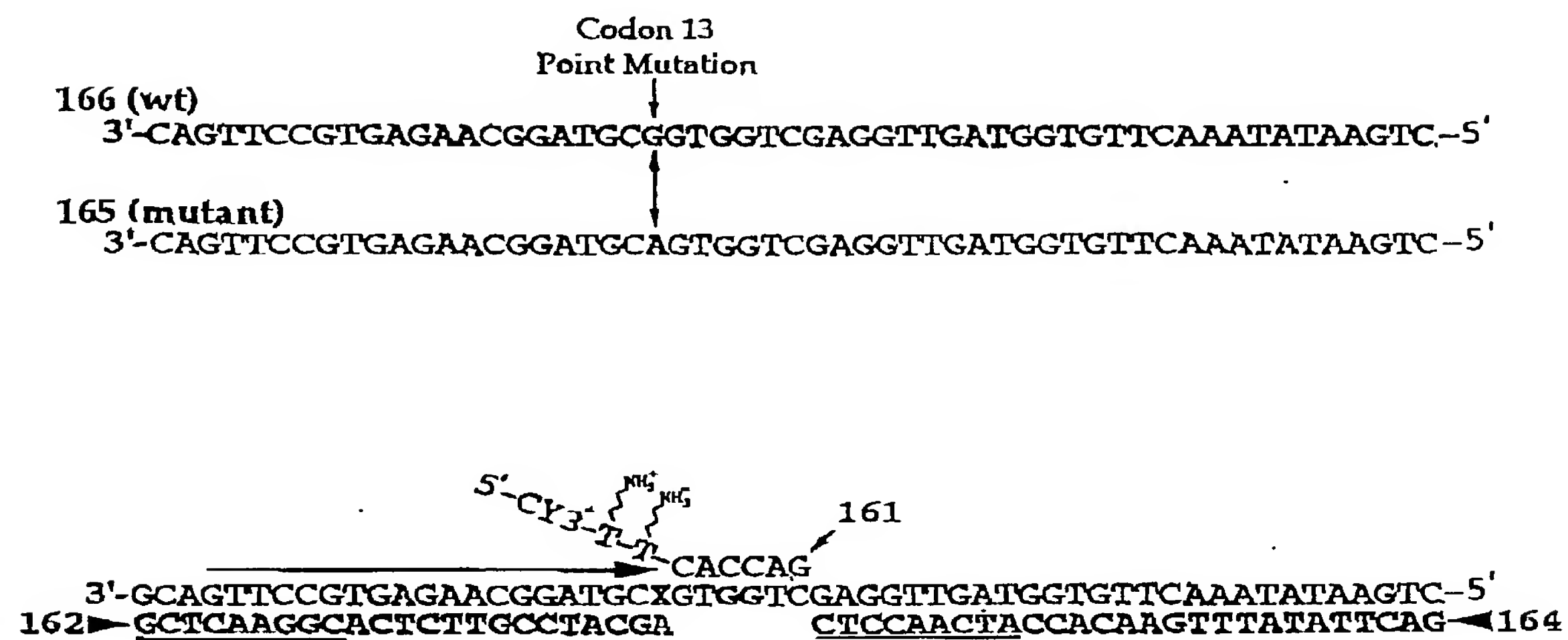
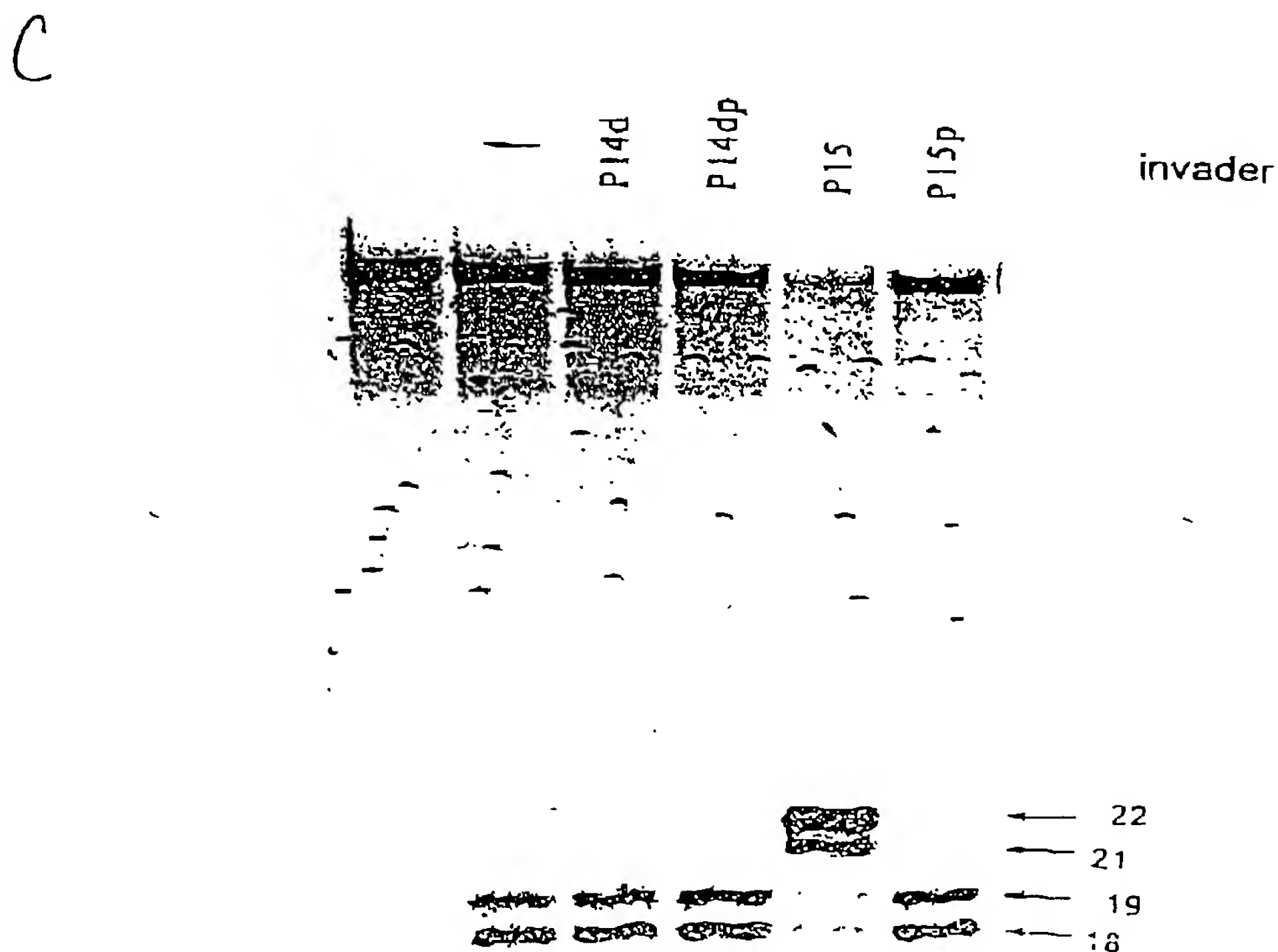
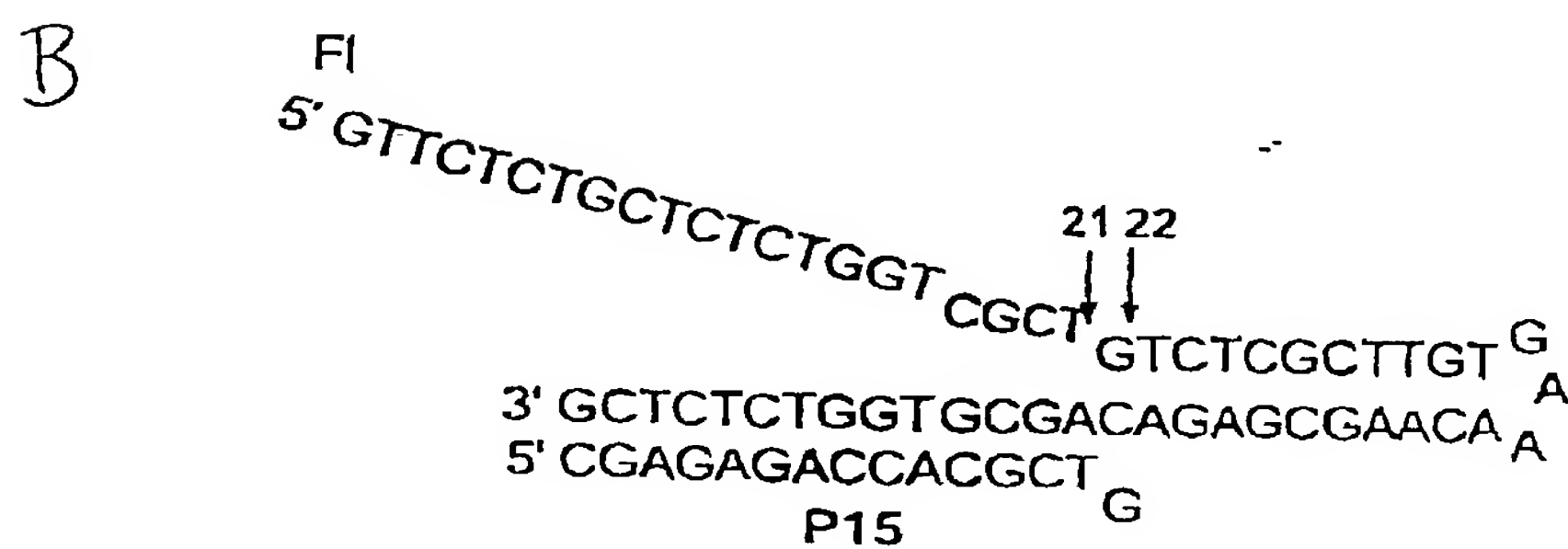
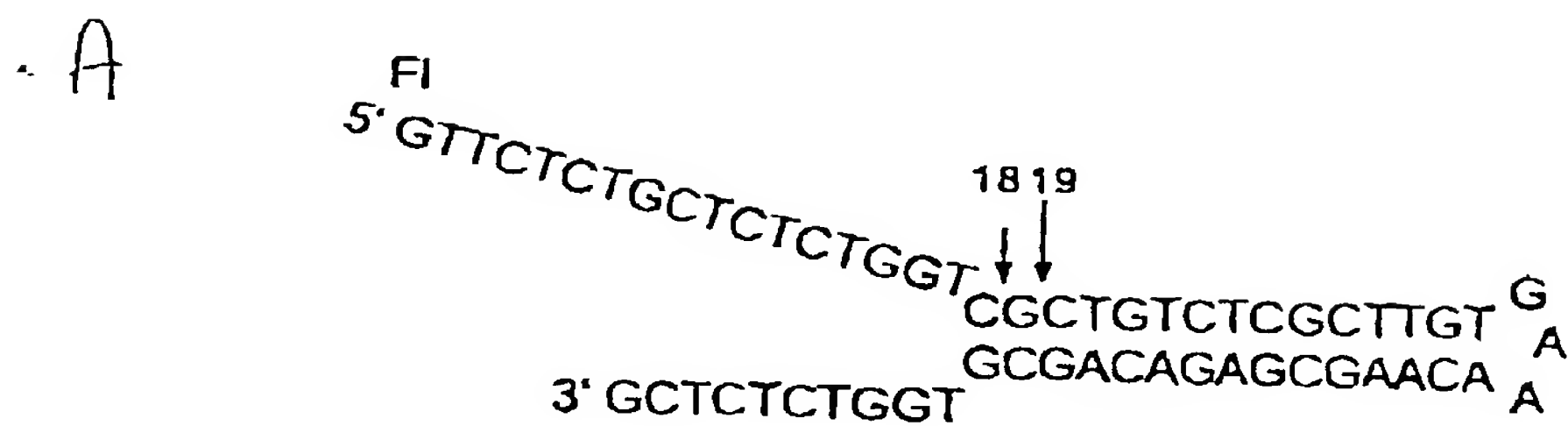


FIGURE 77

Temp	→		47°		50°		53°		56°	
Target	→	—	165	166	165	166	165	166	165	166



FIGURE 78



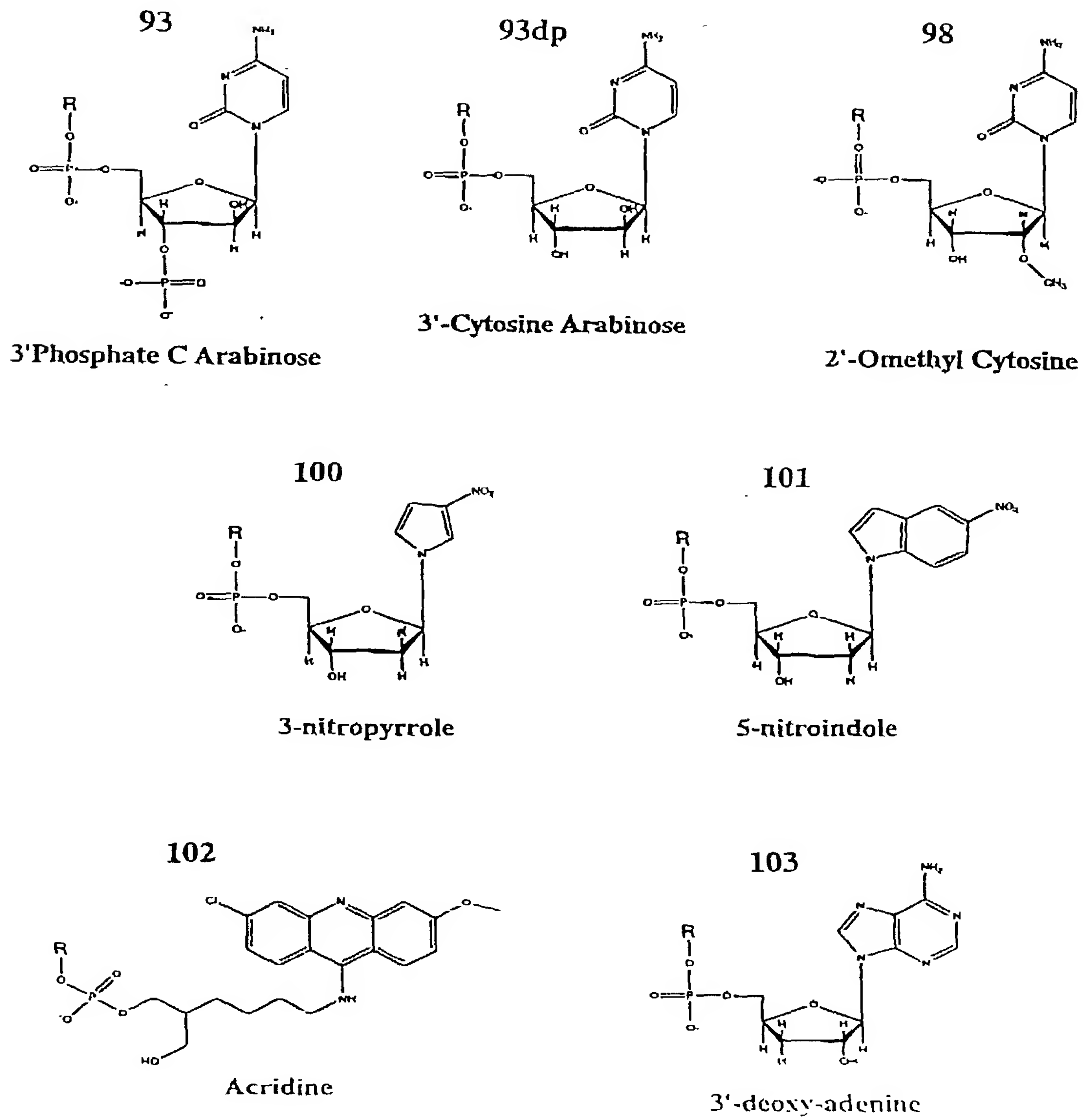


FIGURE 79

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Concentration of Probe w/ and w/o Stacker vs Temp

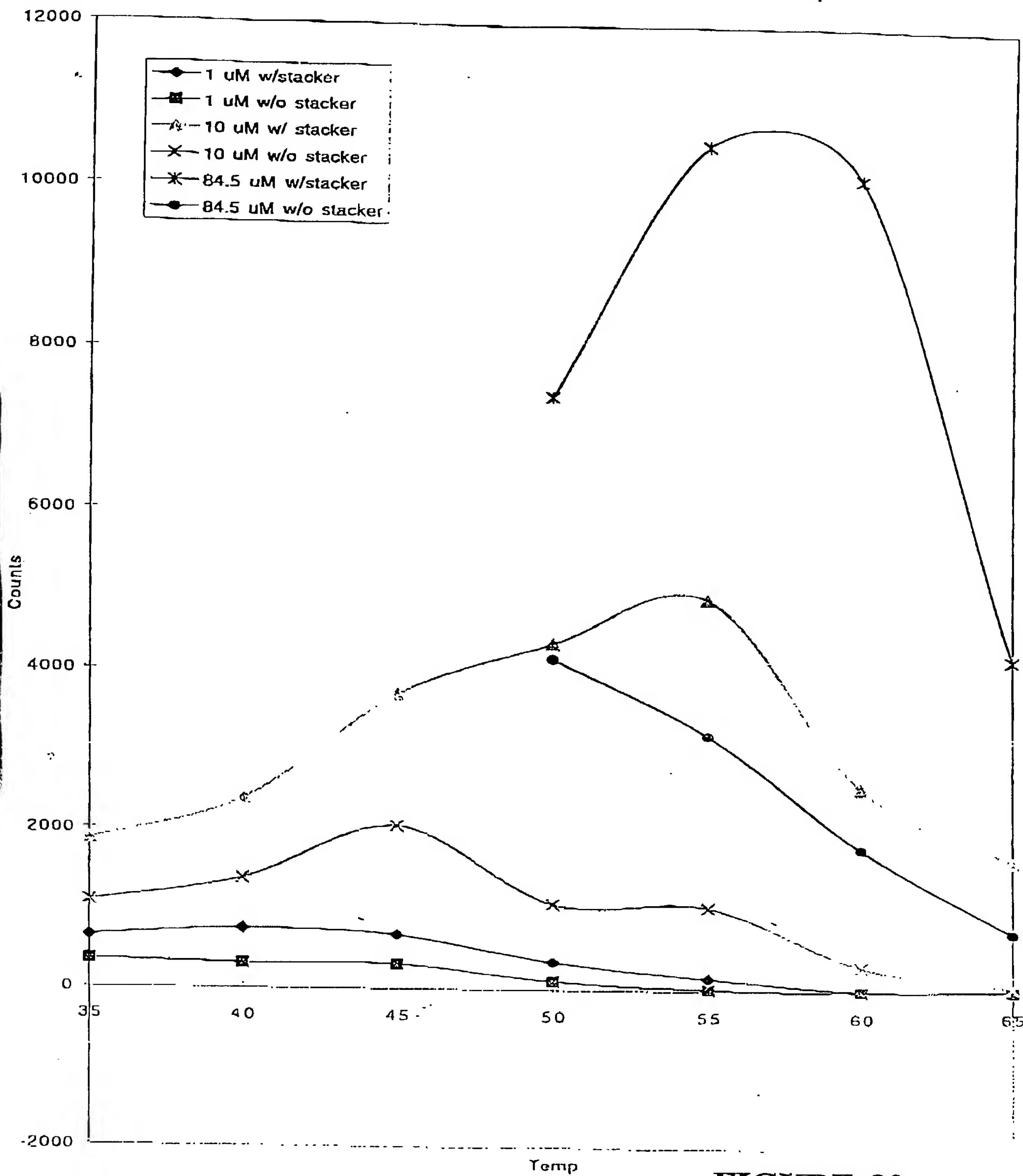


FIGURE 80

FIGURE 81

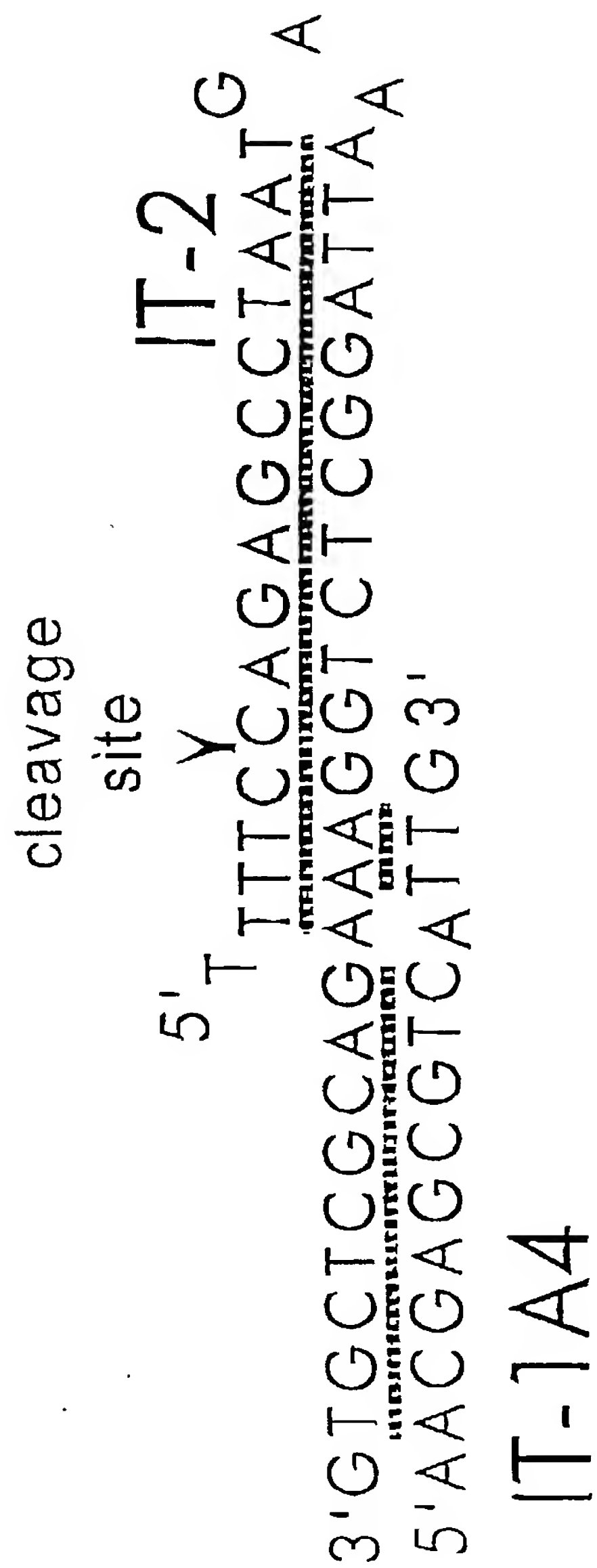
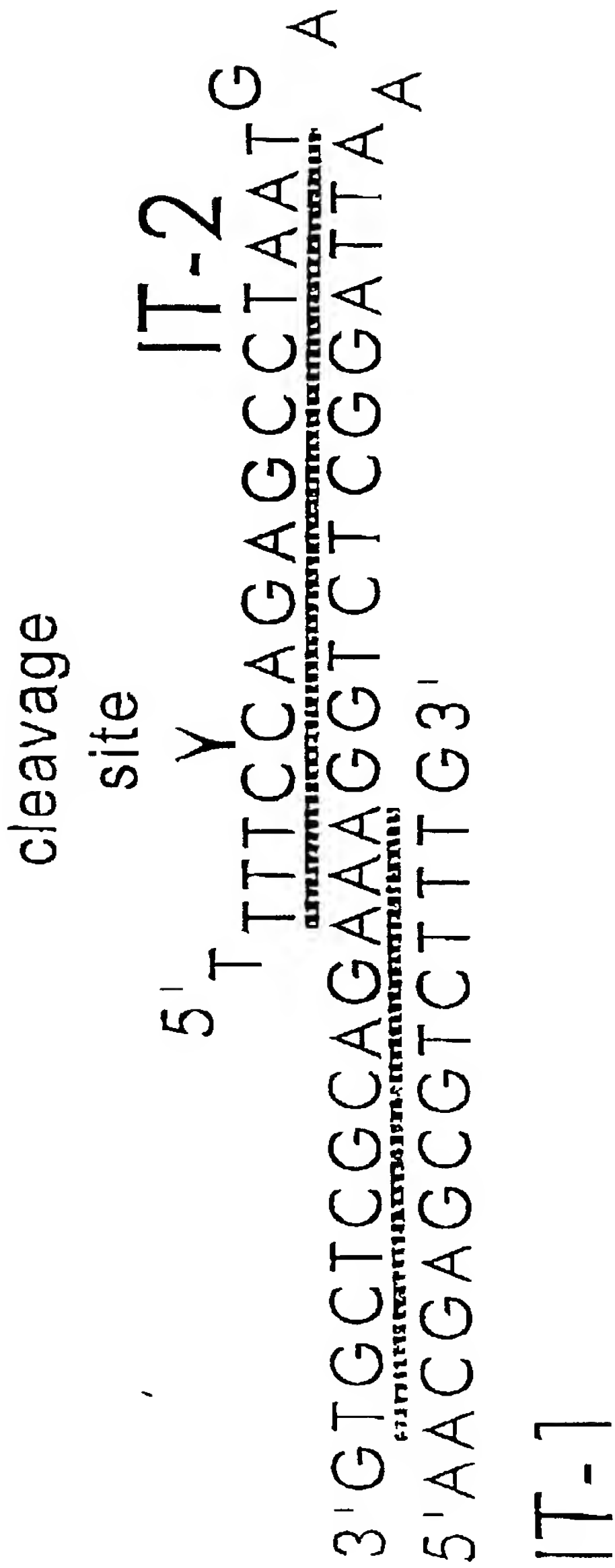


FIGURE 82

1 2 3 4



-Uncut

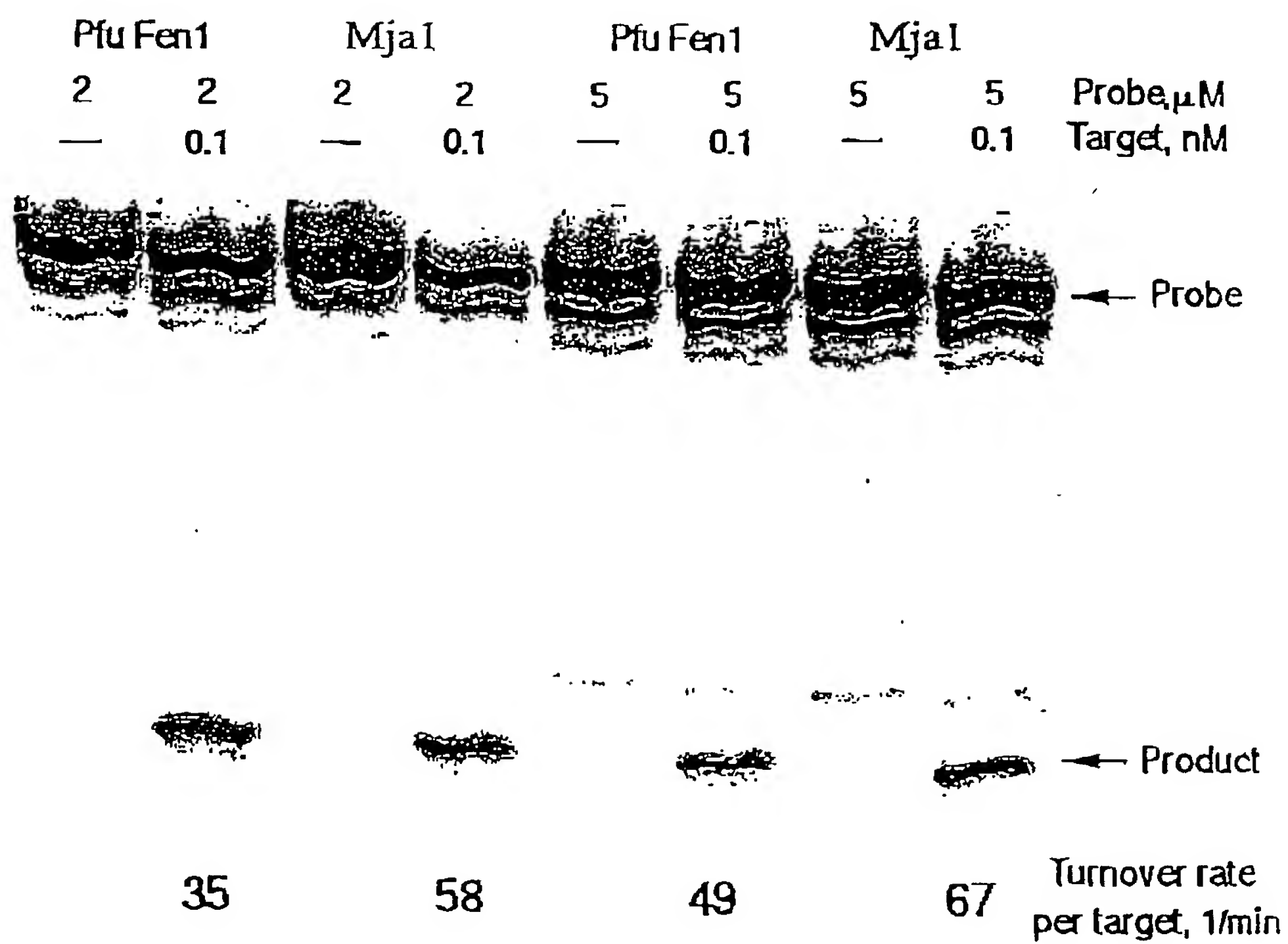
FIGURE 83

FIGURE 84

1 2 3 4 5

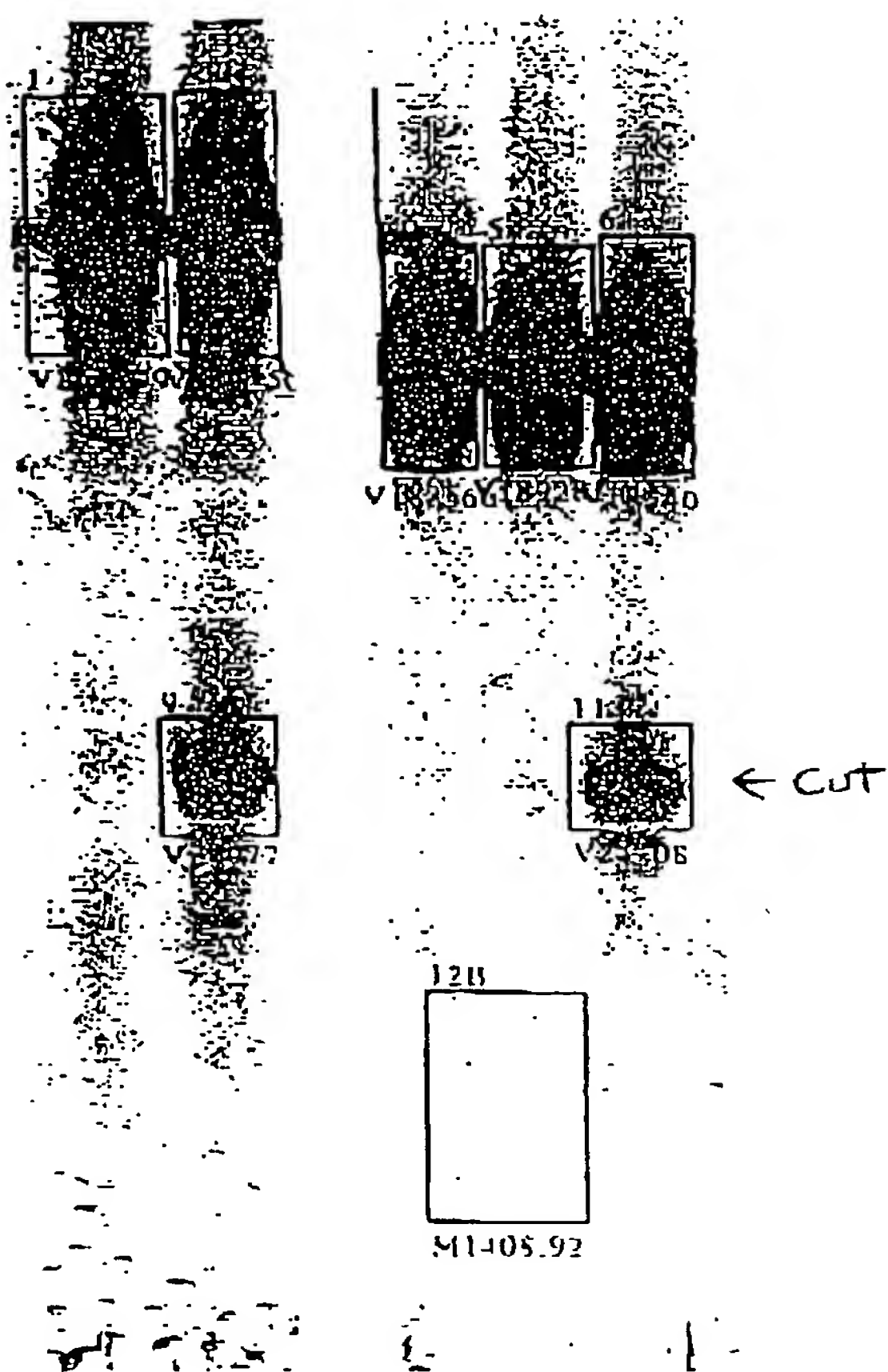


FIGURE 85

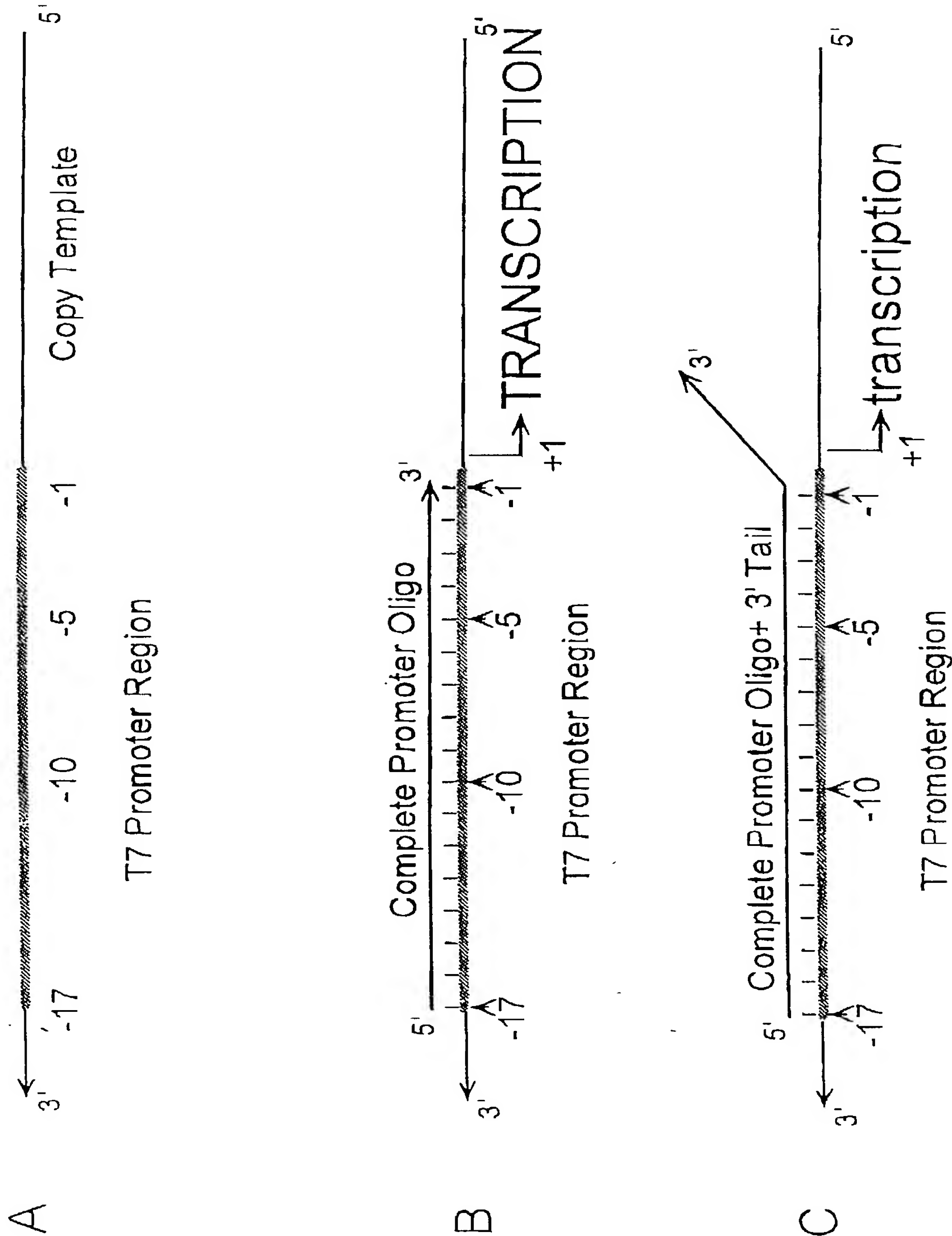




FIGURE 86A

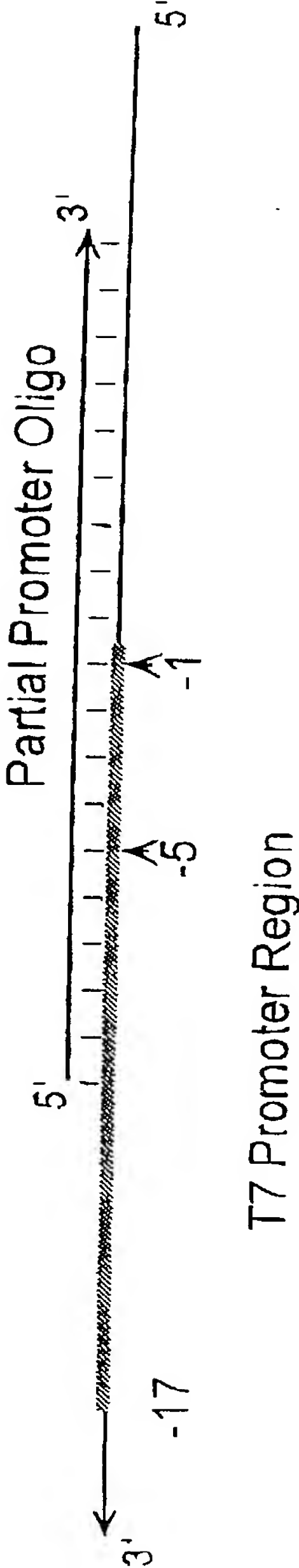


FIGURE 86B

FIGURE 87

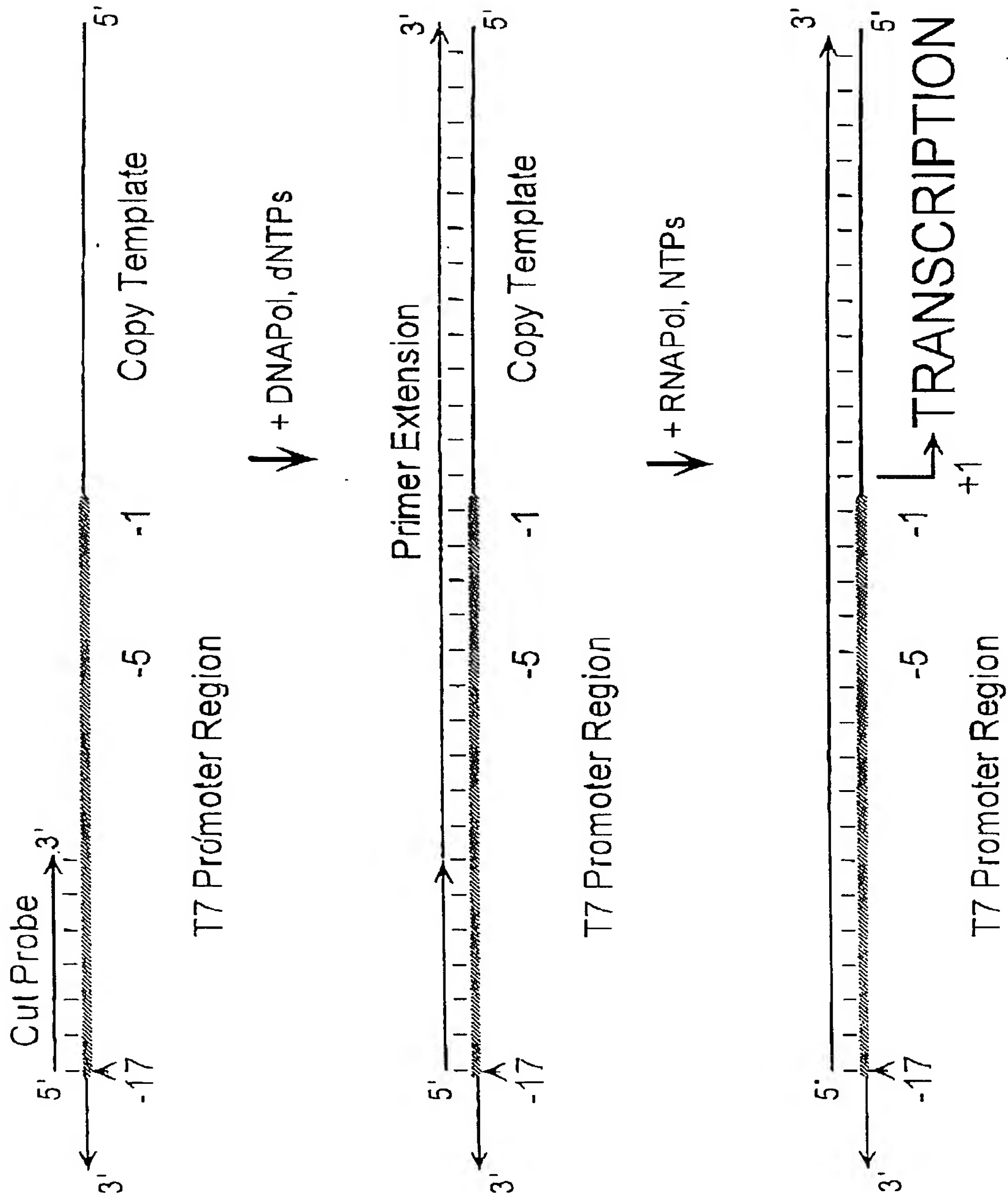


FIGURE 88A

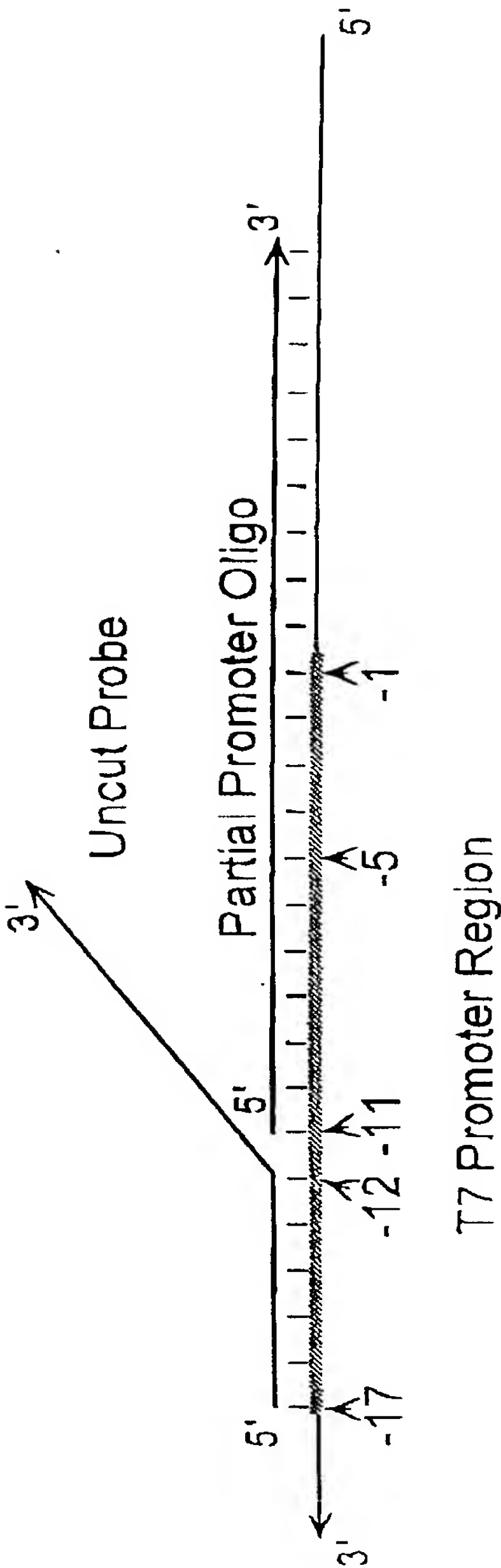
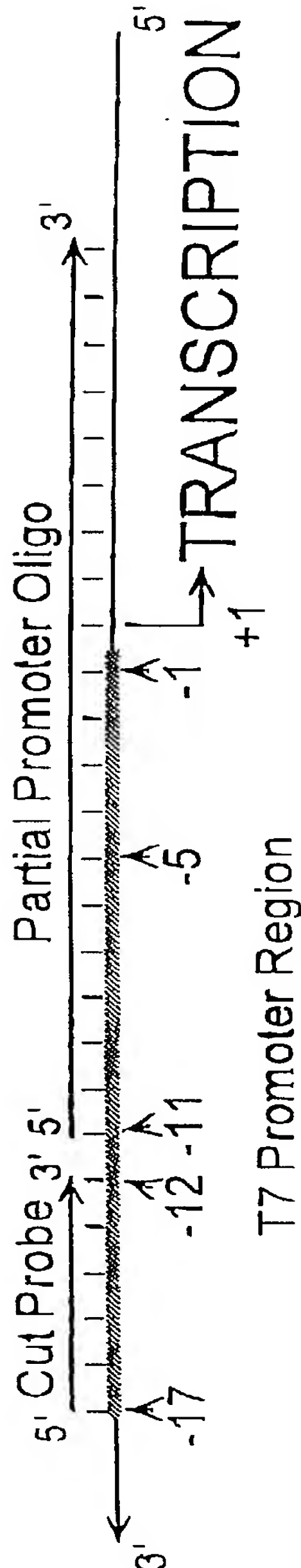
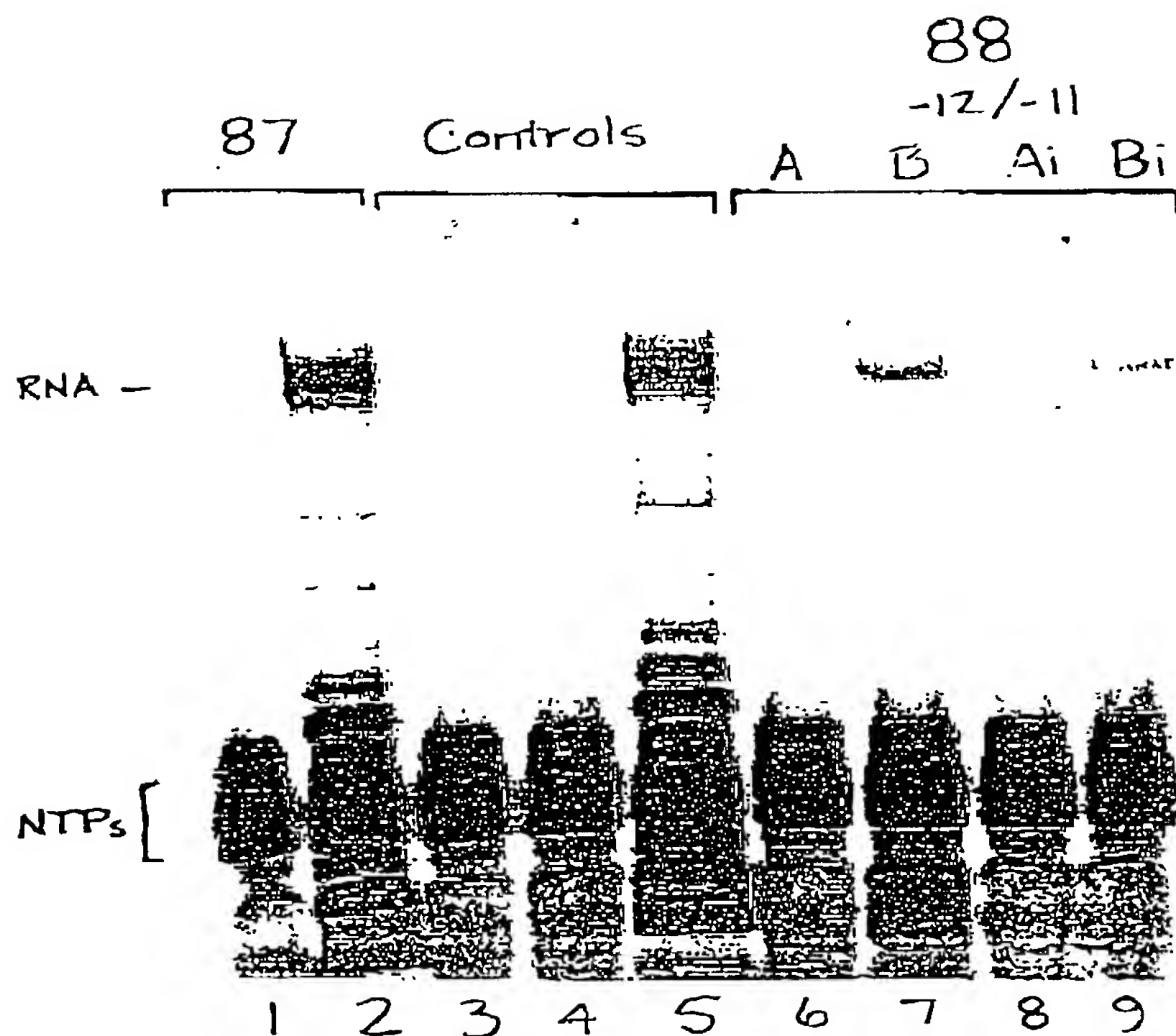


FIGURE 88B



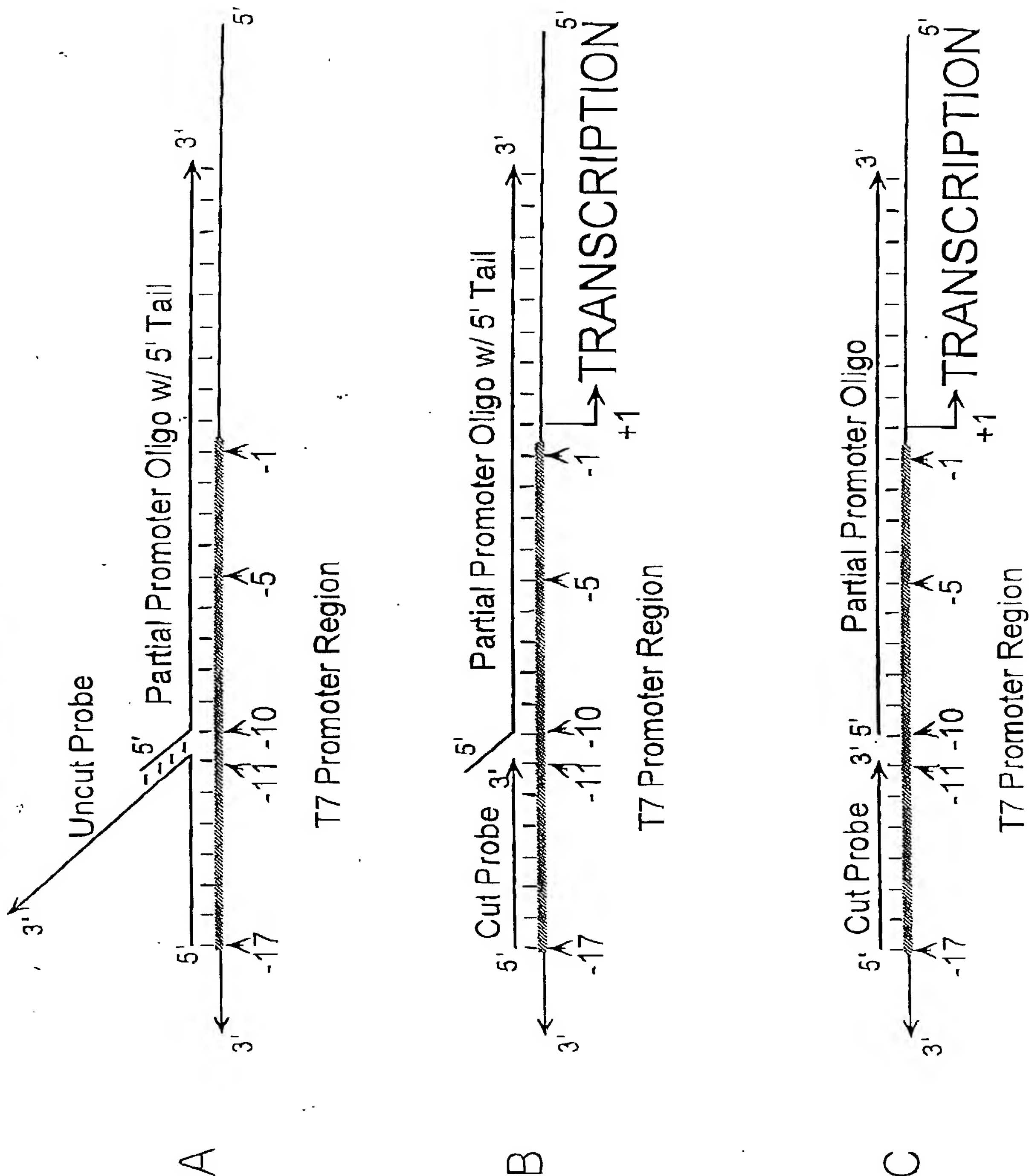
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FIGURE 89



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FIGURE 90



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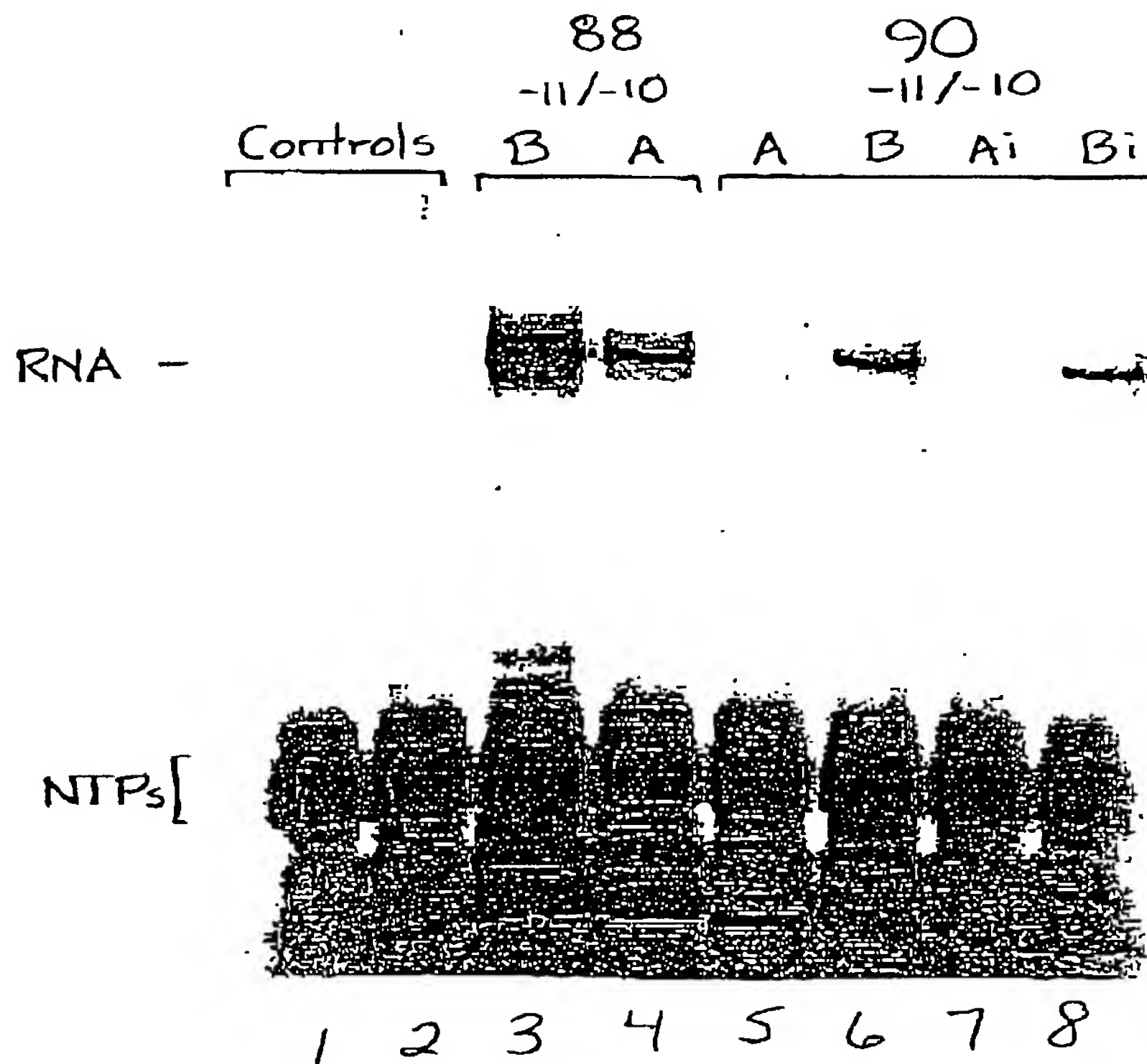


FIGURE 91

FIGURE 92

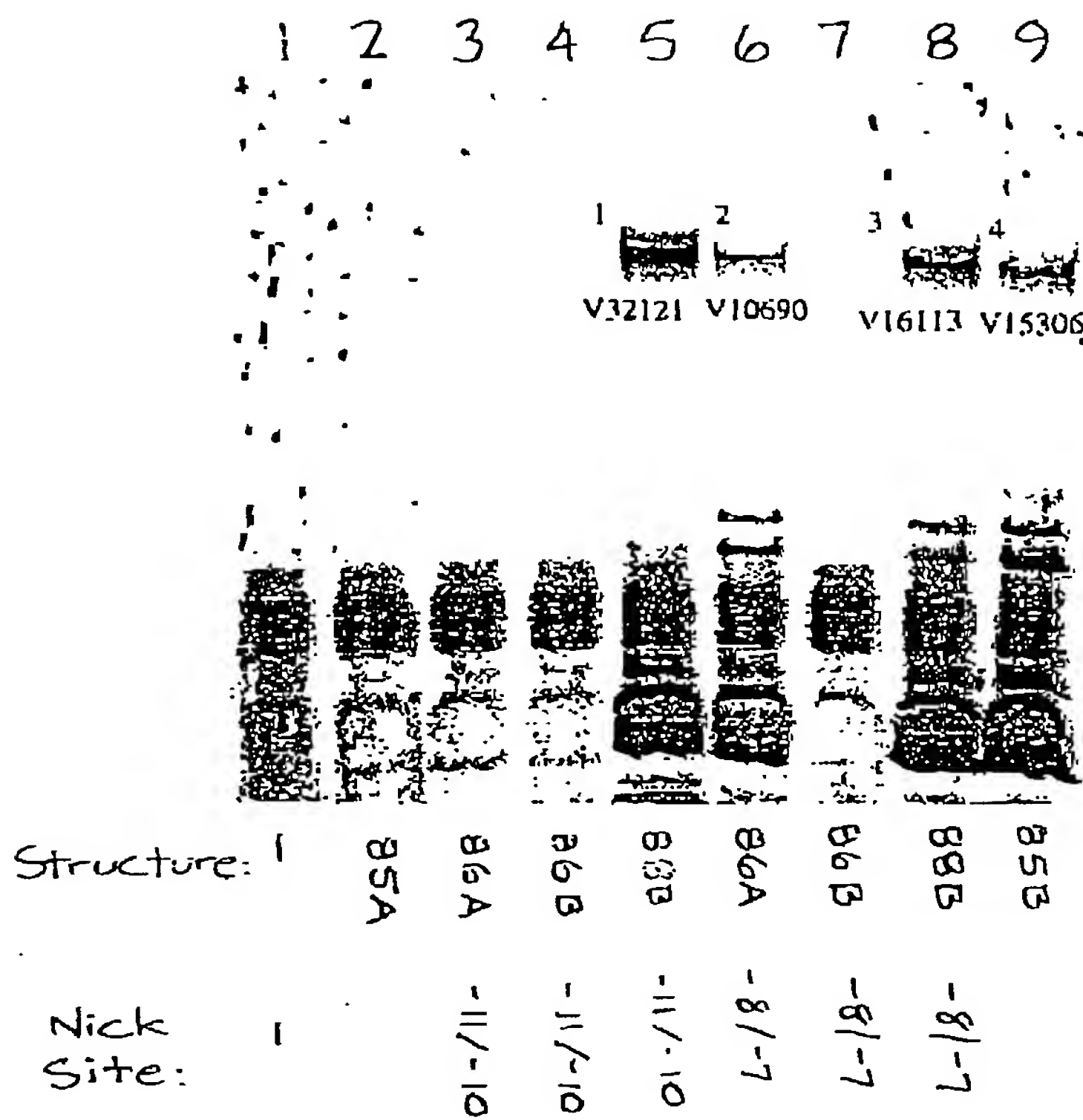
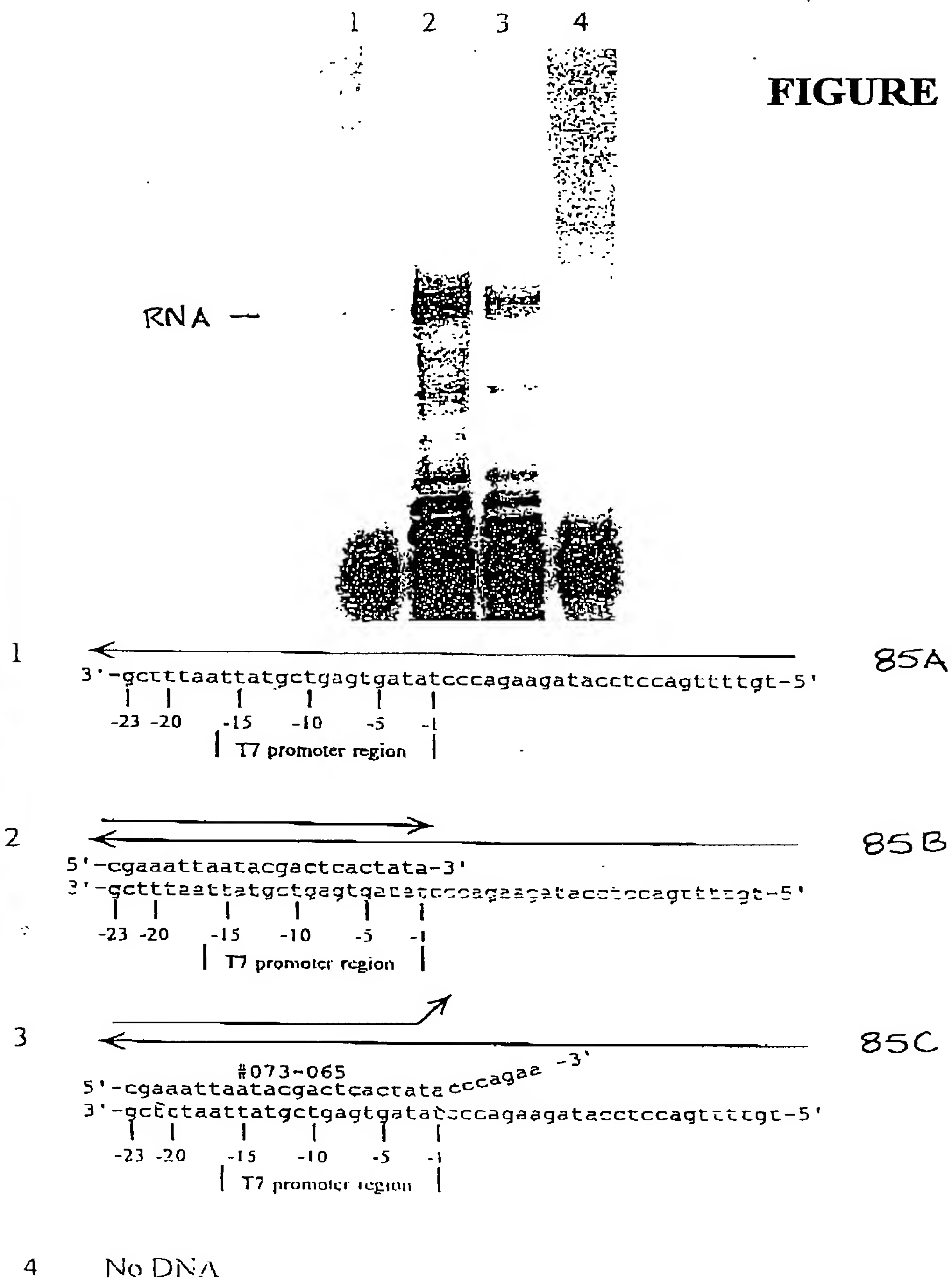
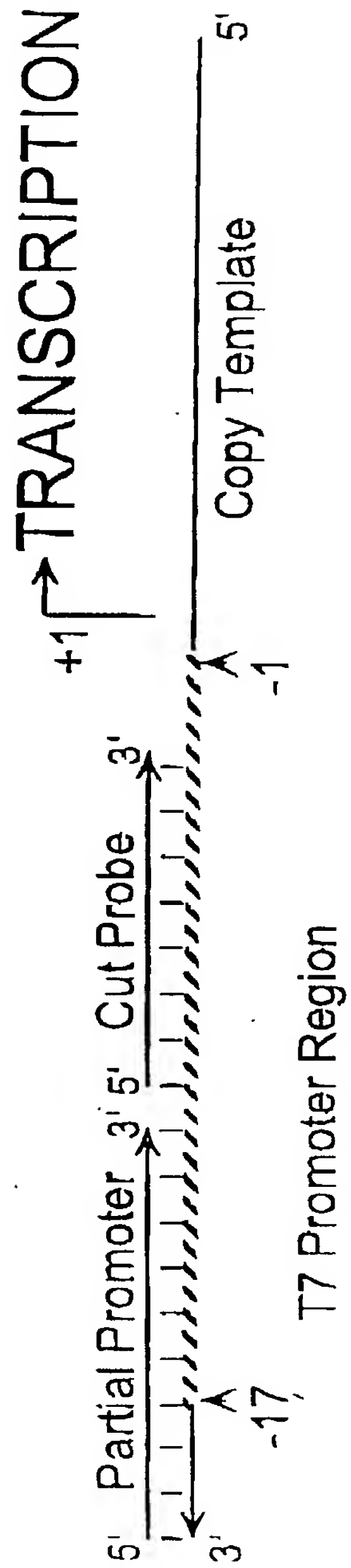


FIGURE 93

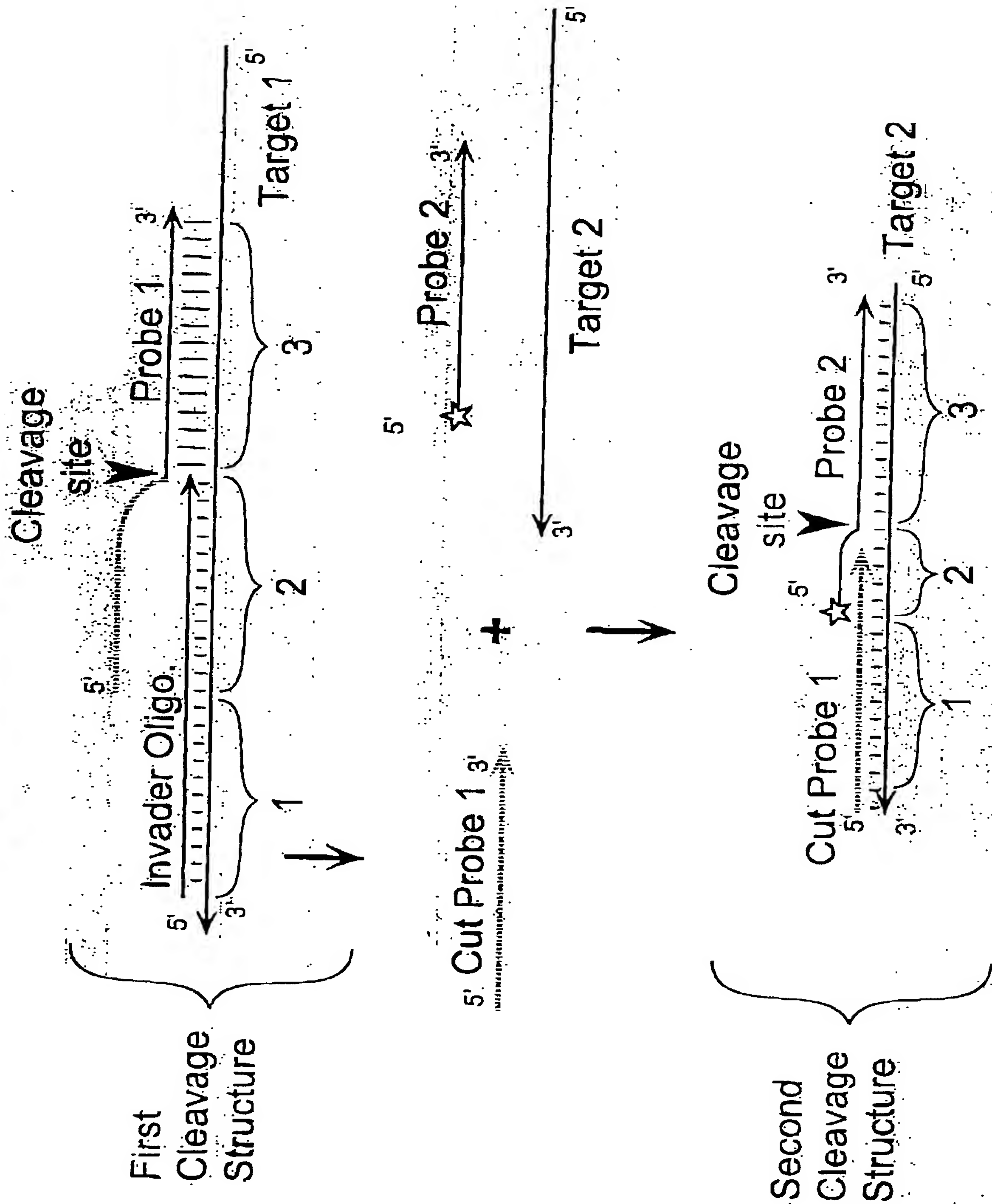


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FIGURE 94



FIGURE



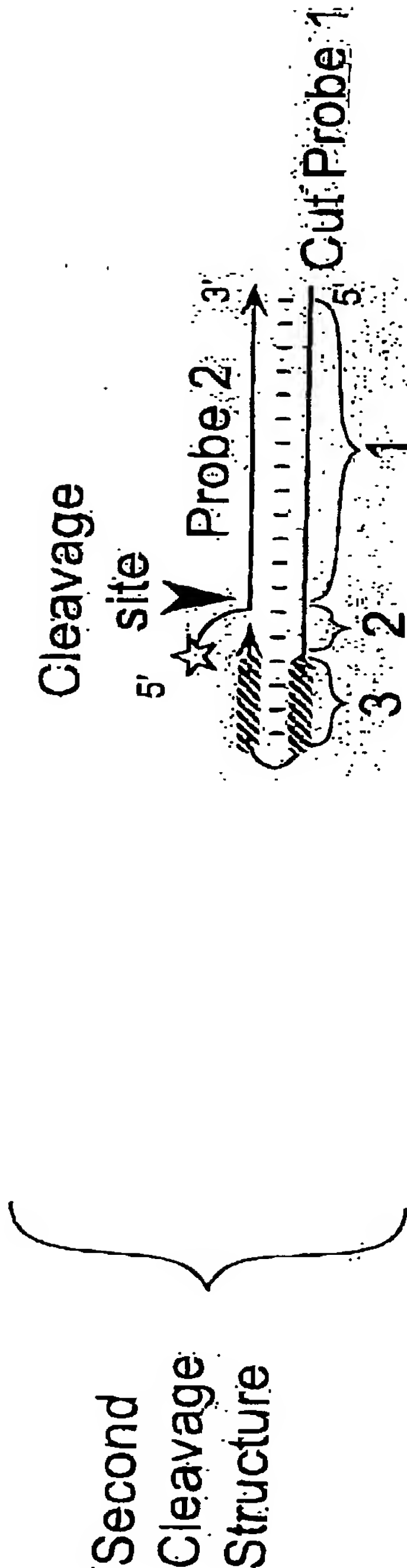
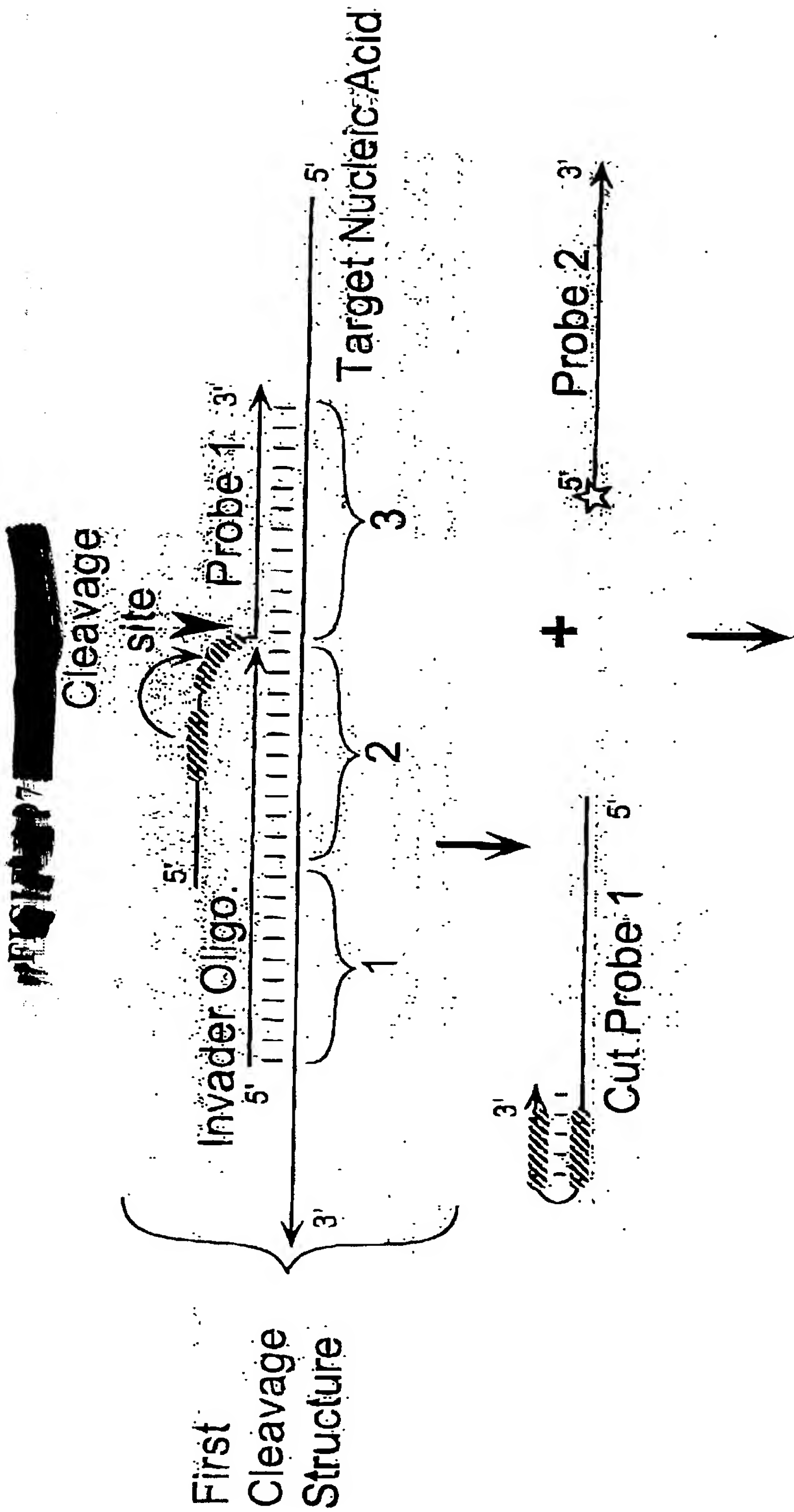


FIGURE 98

PR1 probeCleavage site
↓

5'FITTTTCCAGAGCCTAAT G3'

IT3 Invader-Target

A^A ACGAGCGTCTTT G3'
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTT5'

IT3-8 Invader-Target

A^A AGCGTCTT G3'
G TCGCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-6 Invader-Target

A^A CGTCTT G3'
G GCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-4 Invader-Target

A^A TCCTT G3'
G AGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-3 Invader-Target

A^A CTT G3'
G GAAGGTCTCGGATTAATTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTT5'

115

FIGURE 99

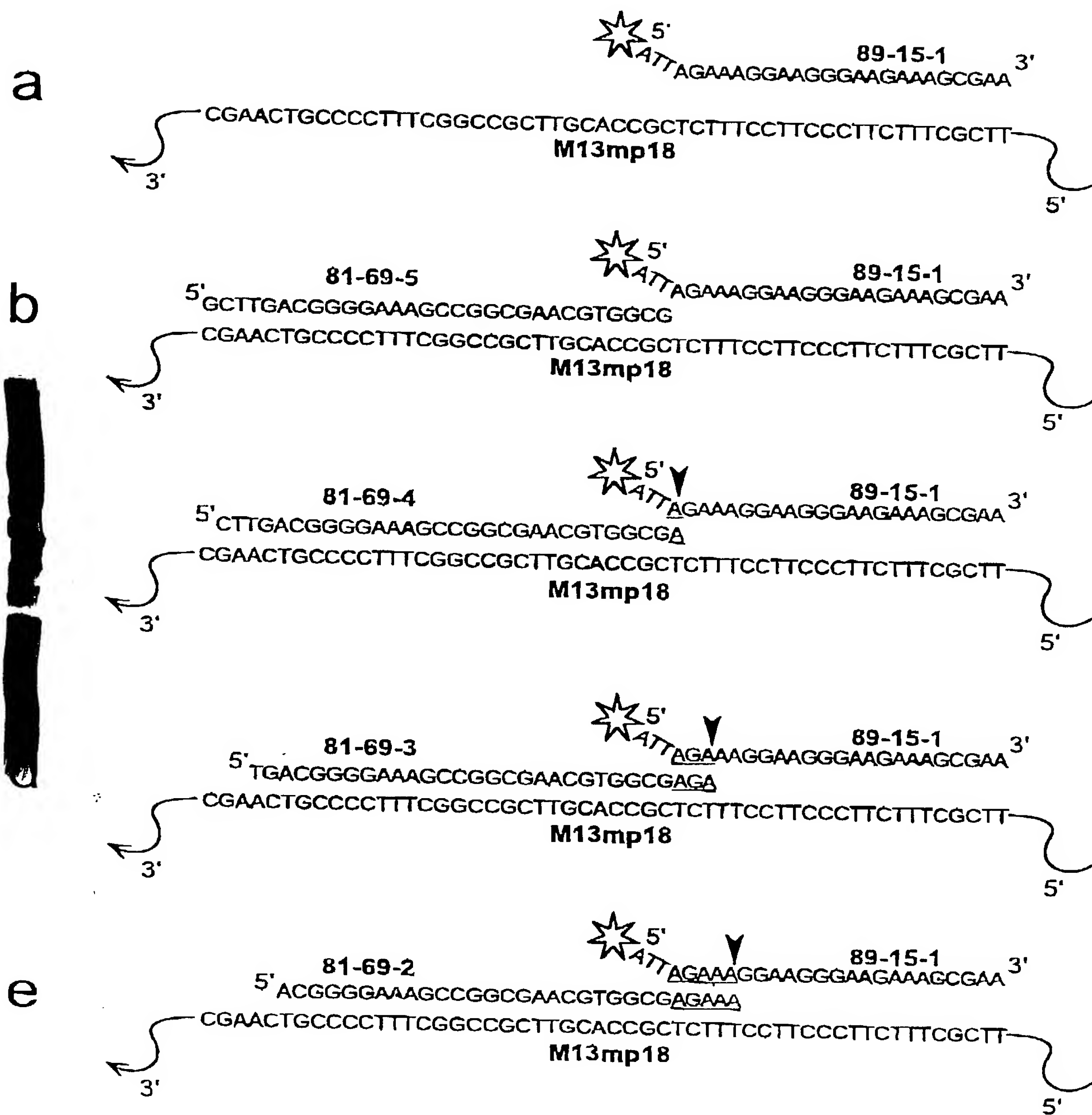
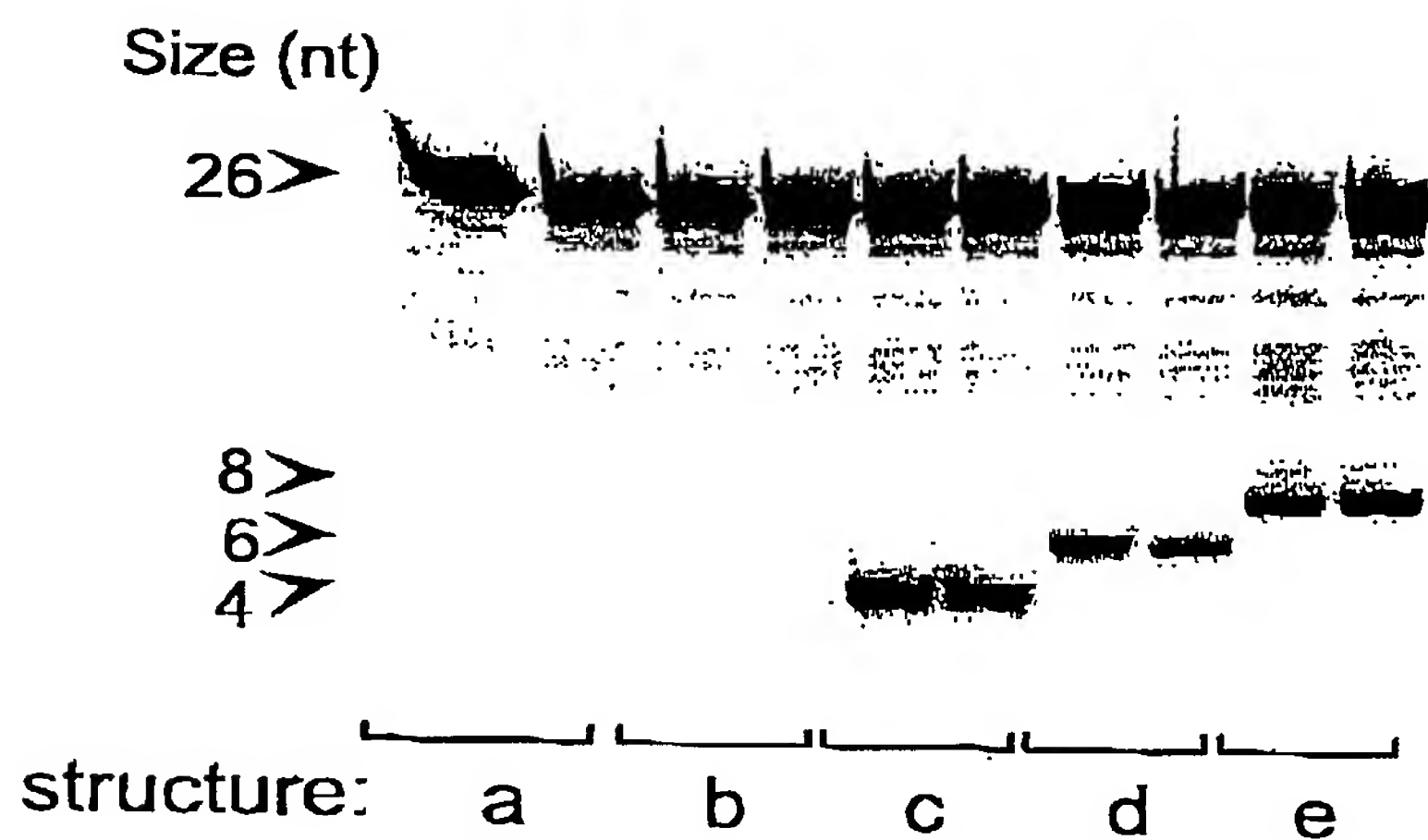


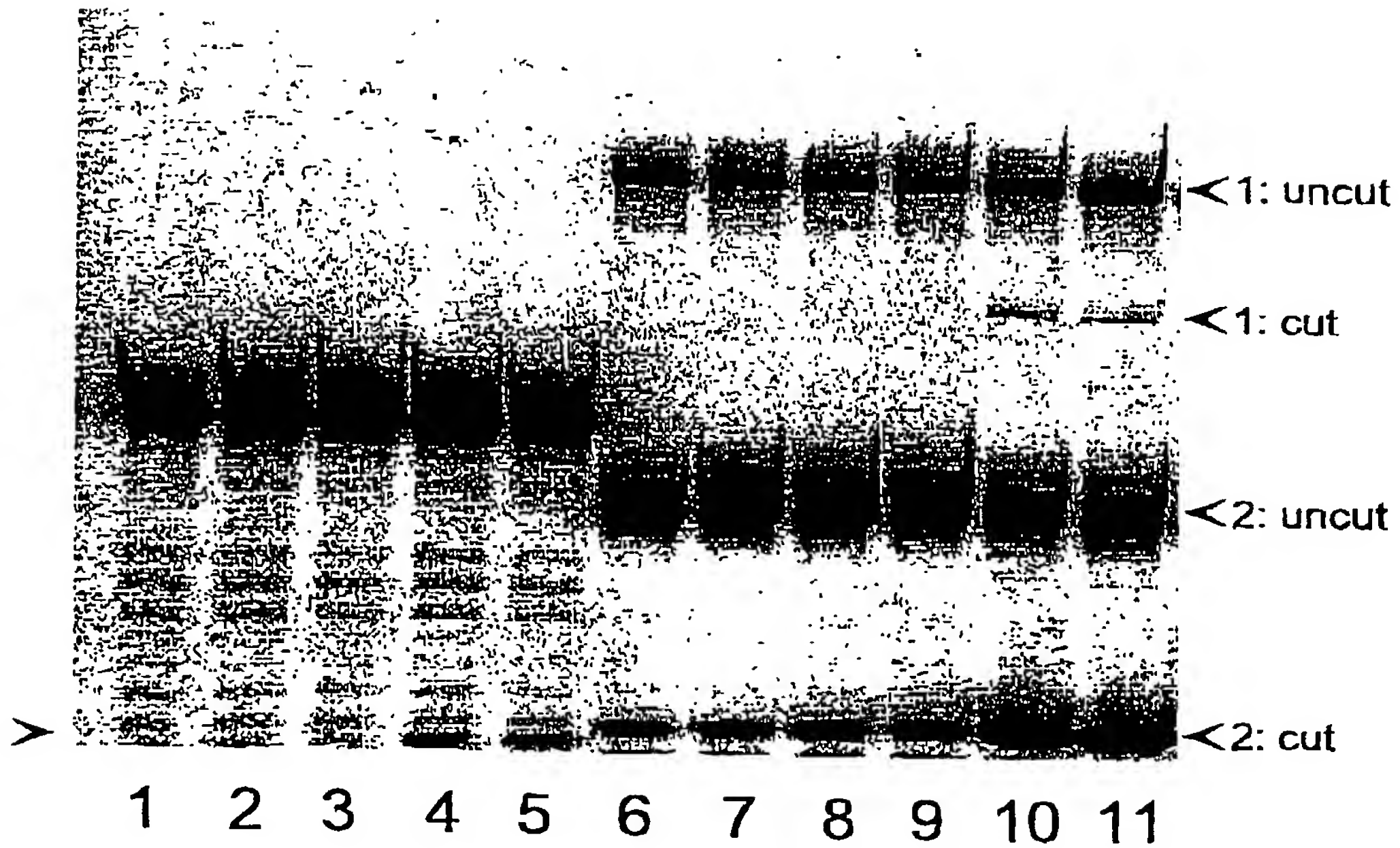
FIGURE 100



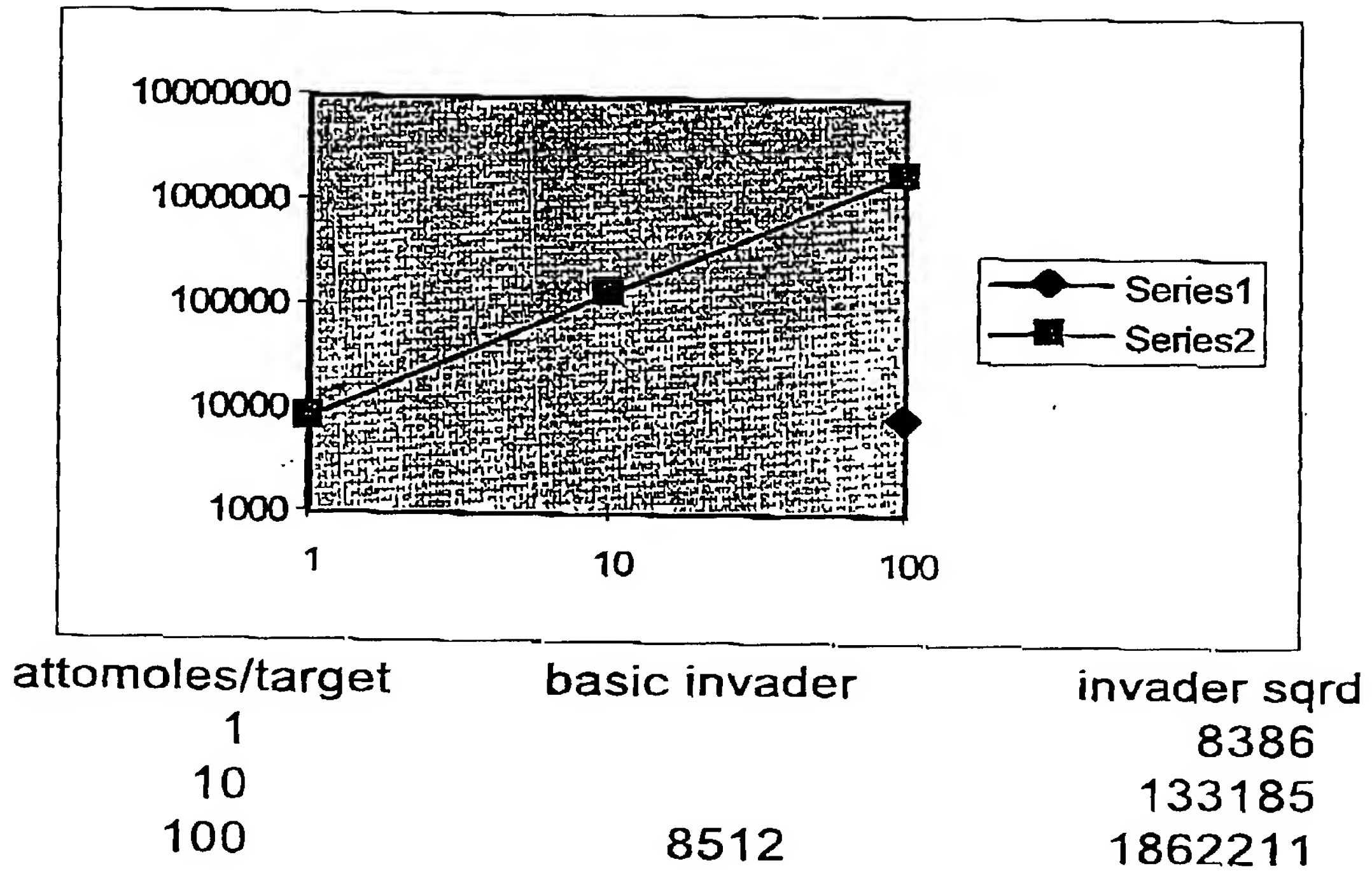
(17)

FIGURE 101

a



b



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FIGURE 102

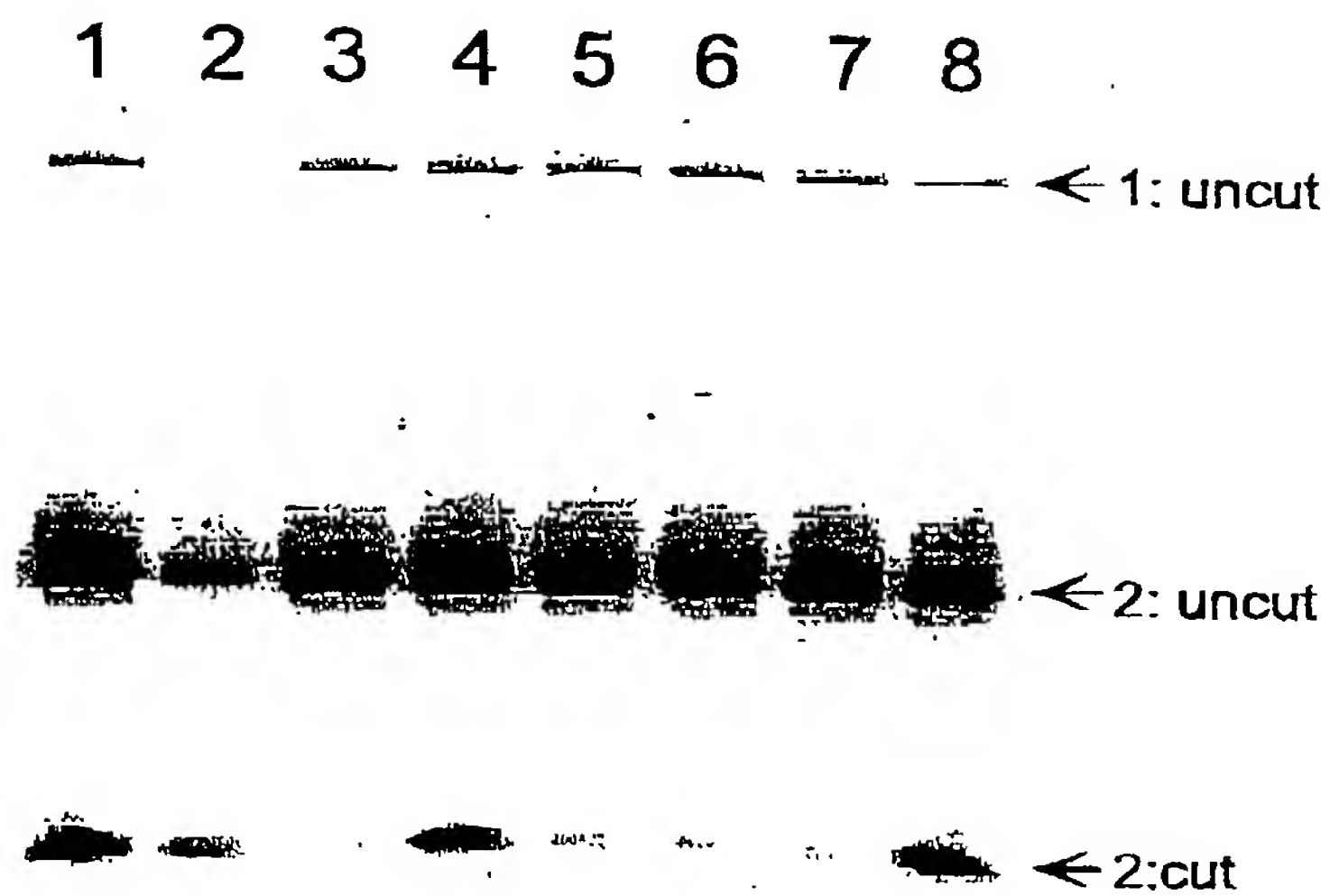
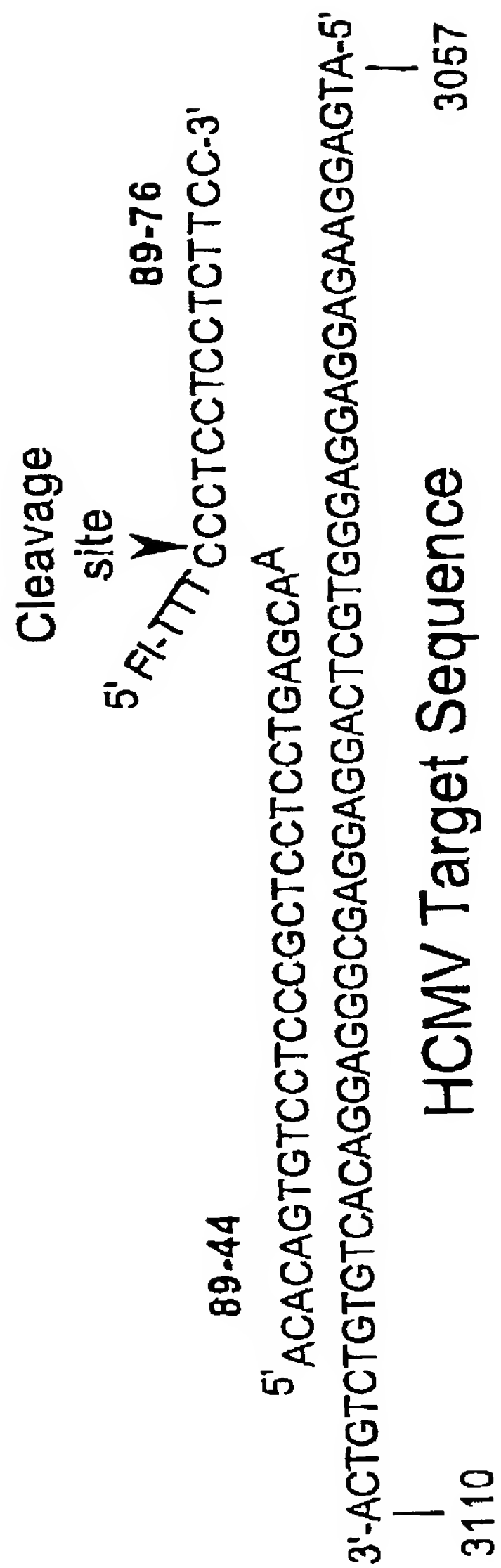


FIGURE 103



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FIGURE 104

